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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: C12N 15/16, C07K 14/575, A61K 38/22, C12N 15/70, 1/21 // (C12N 1/21, C12R 1:19)	A1	(11) International Publication Number: WO 97/24440 (43) International Publication Date: 10 July 1997 (10.07.97)
(21) International Application Number: PCT/US96/20718 (22) International Filing Date: 19 December 1996 (19.12.96) (30) Priority Data: 08/579,494 27 December 1995 (27.12.95) US 08/667,184 20 June 1996 (20.06.96) US (60) Parent Application or Grant (63) Related by Continuation US 08/667,184 (CIP) Filed on 20 June 1996 (20.06.96) (71) Applicant (for all designated States except US): GENENTECH, INC. [US/US]; 460 Point San Bruno Boulevard, South San Francisco, CA 94080 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): DE SAUVAGE, Frederic, J. [BE/US]; 166 Beach Park Boulevard, Foster City, CA 94404 (US). LEVIN, Nancy [US/US]; 900 Ashbury Street #D, San Francisco, CA 94117 (US). VANDLEN, Richard, L. [US/US]; 1015 Haynes Road, Hillsborough, CA 94010 (US).	(74) Agents: DREGER, Ginger, R. et al.; Genentech, Inc., 460 Point San Bruno Boulevard, South San Francisco, CA 94080-4990 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: OB PROTEIN DERIVATIVES HAVING PROLONGED HALF-LIFE (57) Abstract The present invention concerns long half-life derivative of the obesity protein OB. The invention specifically concerns OB protein-immunoglobulin chimeras and polyethylene glycol (PEG)-OB derivatives, which have extended half-life as compared to the corresponding native OB proteins. The invention further relates to methods for appetite and/or weight reduction and for treating other physiological conditions by using the long half-life derivatives of OB.		

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OB PROTEIN DERIVATIVES HAVING PROLONGED HALF-LIFE**Field of the Invention**

The invention concerns long half-life derivatives of the OB protein. In particular, the invention concerns OB protein-immunoglobulin chimeras, and other long half-life derivatives of the OB protein, and compositions comprising and methods for administering them. The invention further relates to a method for treating obesity by administering a long half-life variant of the OB protein, such as, an OB protein-immunoglobulin chimera.

Background of the Invention

Obesity is the most common nutritional disorder which, according to recent epidemiologic studies, affects about one third of all Americans 20 years of age or older. Kuczmarski *et al.*, J. Am. Med. Assoc. **272**, 205-11 (1994). Obesity is responsible for a variety of serious health problems, including cardiovascular disorders, type II diabetes, insulin-resistance, hypertension, hypertriglyceridemia, dyslipoproteinemia, and some forms of cancer. Pi-Sunyer, F.X., Anns. Int. Med. **119**, 655-60 (1993); Colfitz, G.A., Am. J. Clin. Nutr. **55**, 503S-507S (1992). A single-gene mutation (the obesity or "*ob*" mutation) has been shown to result in obesity and type II diabetes in mice. Friedman, Genomics **11**, 1054-1062 (1991). Zhang *et al.*, Nature **372**, 425-431 (1994) have recently reported the cloning and sequencing of the mouse *ob* gene and its human homologue, and suggested that the *ob* gene product may function as part of a signalling pathway from adipose tissue that acts to regulate the size of the body fat depot. Parabiosis experiments performed more than 20 years ago predicted that the genetically obese mouse containing two mutant copies of the *ob* gene (*ob/ob* mouse) does not produce a satiety factor which regulates its food intake, while the diabetic (*db/db*) mouse produces but does not respond to a satiety factor. Coleman and Hummal, Am. J. Physiol. **217**, 1298-1304 (1969); Coleman, Diabetol **9**, 294-98 (1973). Recent reports by three independent research teams have demonstrated that daily injections of recombinant OB protein inhibit food intake and reduce body weight and fat in grossly obese *ob/ob* mice but not in *db/db* mice (Pellemounter *et al.*, Science **269**, 540-43 [1995]; Halaas *et al.*, Science **269**, 543-46 [1995]; Campfield *et al.*, Science **269**, 546-49 [1995]), suggesting that the *ob* protein is such a satiety factor as proposed in early cross-circulation studies. The results of these first studies leave many questions unanswered, and show a number of as yet unresolved discrepancies. For example, while modest effects of daily injections of the *ob* protein on food intake and body weight were reported in lean mice, there was a significant reduction in body fat as assessed by carcass composition in one (Halaas *et al.*, *supra*) but not in another (Pellemounter *et al.*, *supra*) of these reports, despite equivalent decreases in body weight. Furthermore, Pellemounter *et al.*, *supra* observed that, for reasons unknown, *ob/ob* mice treated with a 0.1 mg/kg/day dose of the OB protein actually increased their body weight by 17.13 %, while the weight reduction in the obese mice that received a 1 mg/kg/day dose of *ob* was rather moderate. The receptor or receptors of the *ob* protein are as of yet unidentified. While the existence of peripheral receptors cannot be ruled out at this time, the recent report that an increased

- expression of the *ob* gene in adipose tissue of mice with hypothalamic lesions does not result in a lean phenotype suggests that the OB protein does not act directly on fat cells. Maffei *et al.*, Proc. Natl. Acad. Sci. **92**, 6957-60 (1995). Researchers suggest that at least one OB receptor is localized in the brain. The identification and expression cloning of a leptin receptor (OB-R) was reported by Tartaglia *et al.*, Cell **83**, 1263-71 (1995).
- 5 Various isoforms of a leptin receptor are described by Cioffi *et al.*, Nature **2**, 585-89 (1996). A human hematopoietin receptor, which might be a receptor of the OB protein, is described in PCT application Publication No. WO 96/08510, published 21 March 1996. A receptor of the OB protein is disclosed in Tartaglia *et al.*, Cell **83**, 1263-71 (1995).

Summary of the Invention

- 10 The present invention is based on the observation that the OB protein is significantly more effective at reducing body weight and adipose tissue weight when delivered as a continuous subcutaneous infusion than when the same dose is delivered as a daily subcutaneous injection. The invention is further based on the unexpected finding that a chimeric protein, in which the OB polypeptide is fused to an immunoglobulin constant domain, is strikingly more potent in reducing the body weight and adipose depots than native human
- 15 OB, when both proteins are administered by subcutaneous injection once a day. The latter observation is particularly surprising since the OB protein-immunoglobulin chimera due to its large molecular weight, is not expected to be able to cross the blood-brain barrier, and reach the OB receptor which has been believed to be located in the brain.

- In one aspect, the invention concerns long half-life derivatives of an OB protein capable of reducing
- 20 body weight and/or food intake in an individual treated. The invention further concerns compositions containing such derivatives, and their administration for reducing body weight and/or food intake.

- In another aspect, the invention concerns chimeric polypeptides comprising an OB protein amino acid sequence capable of binding to a native OB receptor linked to an immunoglobulin sequence (briefly referred to as OB-immunoglobulin chimeras or immunoadhesins). In a specific embodiment, the chimeric polypeptides
- 25 comprise a fusion of an OB amino acid sequence capable of binding a native OB receptor, to an immunoglobulin constant domain sequence. The OB portion of the chimeras of the present invention preferably has sufficient amino acid sequences from a native OB protein to retain the ability to bind to and signal through a native OB receptor. Most preferably, the OB protein retains the ability to reduce body weight when administered to obese human or non-human subjects. The OB polypeptide is preferably human, and the fusion is preferably with an
- 30 immunoglobulin heavy chain constant domain sequence. In a particular embodiment, the association of two OB polypeptide-immunoglobulin heavy chain fusions (e.g., via covalent linkage by disulfide bond(s)) results in a homodimeric immunoglobulin-like structure. An immunoglobulin light chain may further be associated with one or both of the OB-immunoglobulin chimeras in the disulfide-bonded dimer to yield a homotrimeric or homotetrameric structure.

- 35 The invention further concerns nucleic acid encoding chimeric polypeptide chains of the present invention, expression vectors containing DNA encoding such molecules, transformed host cells, and methods for the production of the molecules by cultivating transformant host cells.

Although the long half-life derivatives of the present invention are particularly useful for reducing body weight and/or food intake, they can generally be used for the treatment of conditions associated with the abnormal expression or function of the OB gene and/or to elicit biological responses mediated by an OB receptor. Thus, the OB derivatives of the present invention may be used to treat bulimia, to reduce insulin levels, e.g. in Type I or II diabetic patients, and as mitogens of various cell types expressing an OB receptor. All these and related uses are within the scope of the present invention.

In another embodiment, the invention concerns the purification of an OB receptor by using an OB protein-immunoglobulin chimera.

Brief Description of the Figures

Figure 1 top -- Lean female mice were treated with murine OB protein either as a continuous subcutaneous infusion or daily subcutaneous injections. The data shown are the mean body weight of each group, in grams, $n = 4$ mice/point.

Figure 1 bottom -- The mean weight of the retroperitoneal fat pads are shown. Continuous subcutaneous infusions of the OB protein were also more effective than daily subcutaneous injections at reducing adipose tissue weight.

Figure 2 top -- Obese female *ob/ob* mice were treated with human OB protein (hOB) or with a human OB-IgG-1 fusion protein (hOB-IgG-1). The data shown are the mean change in body weight for each treatment group from the first to the last day of experiment, in grams, $n = 3$ mice/bar except for the hOB 0.19 mg/kg/day by injection group, where $n = 4$, and PBS injection group, where $n = 1$.

Figure 2 bottom -- The data shown were the mean food intake for each treatment group for the six 24 hour periods of the experiment, in grams/mouse/day, $n = 1$ /bar.

Figure 3 top and bottom -- Obese (*ob/ob*) female mice were treated with either hOB or the hOB-IgG-1 fusion protein by daily subcutaneous injections for 7 days. The data are depicted as in Figure 2, with $n = 4$ for all treatment groups.

Figure 4 top -- Obese female *ob/ob* mice were treated with human protein (hOB) or with PEG-hOB. The data shown are the mean change in body weight for each treatment group from the first to the last day of experiment, in grams, $n = 3-4$ mice/bar except for the PBS injection group, where $n = 1$. The materials were injected daily subcutaneously. The "PEG 1X" and "PEG 2X" refer to the ratio of the PEG reagent to protein in the preparation of the molecule.

Figure 4 bottom -- The data shown were the mean food intake for each treatment group for the six 24 hour periods of the experiment, in grams/mouse/day, $n = 3-4$ /bar.

Figure 5 -- Obese (*ob/ob*) female mice were treated with either the hOB-IgG fusion protein, native hOB, or hCD4-IgG by daily subcutaneous injections for 7 days. $n = 6$ for all treatment groups, except hOB at 3.8 mg/kg/d, where $n = 2$. Again it was observed that the fusion protein was more effective than the native hOB protein at reducing body weight (top and middle panels) and food intake (bottom panel).

Figure 6 -- The nucleotide sequence (SEQ. ID. NO:1) and the amino acid sequence (SEQ. ID. NO:2) of the human OB-IgG-1 chimera of Example 1.

Detailed Description of the Invention

A. Definitions

The term "obesity" is used to designate a condition of being overweight associated with excessive bodily fat. The desirable weight for a certain individual depends on a number of factors including sex, height, age, overall built, etc. The same factors will determine when an individual is considered obese. The determination of an optimum body weight for a given individual is well within the skill of an ordinary physician.

The phrase "long half-life" and grammatical variants thereof, as used in connection with OB derivatives, concerns OB derivatives having a longer plasma half-life and/or slower clearance than a corresponding native OB protein. The long half-life derivatives preferably will have a half-life at least about 1.5-times longer than a native OB protein; more preferably at least about 2-times longer than a native OB protein, more preferably at least about 3-time longer than a native OB protein. The native OB protein preferably is that of the individual to be treated.

The terms "OB", "OB polypeptide", "OB protein" and their grammatical variants are used interchangeably and refer to "native" or "native sequence" OB proteins (also known as "leptins") and their functional derivatives. The OB polypeptides have the typical structural features of cytokines, i.e. polypeptides released by one cell population which act on another cell as intercellular mediators, such as, for example, growth hormones, insulin-like growth factors, interleukins, insulin, glycoprotein hormones such as, follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), tumor necrosis factor- α and - β (TNF- α and - β), nerve growth factors, such as NGF- β , PDGF, transforming growth factors (TGFs) such as, TGF- α and TGF- β , insulin-like growth factor-1 and -2 (IGF-1 and IGF-2), erythropoietin, osteoinductive factors, interferons (IFNs) such as, IFN- α , IFN- β and IFN- γ , colony stimulating factors (CSFs) such as, M-CSF, GM-CSF, and G-CSF, interleukins (ILs) such as, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8 and other polypeptide factors.

The terms "native" and "native sequence" OB polypeptide are used to refer to an OB polypeptide from any animal species (e.g. human, murine, rabbit, cat, cow, sheep, chicken, porcine, equine, etc.), as occurring in nature, including naturally-occurring alleles, deletion, substitution and/or insertion variants, as currently known or as might be identified in the future, provided that they retain the ability to bind to and, preferably, signal through the OB receptor. Thus, a native human OB polypeptide includes the amino acid sequence between the N-terminus and the cysteine (Cys) at position 167 of the amino acid sequence shown in Figure 6 (see also SEQ. ID. NO: 2 and Figure 6 of Zhang *et al.*, supra), and naturally occurring variants of this protein, as currently known or might be identified in the future. Similarly, a "native" or "native sequence" murine OB polypeptide has the amino acid sequence shown in Figure 6 of Zhang *et al.*, supra, and naturally occurring variants of that polypeptide, as currently known or might be identified in the future. The definition specifically includes variants with or without a glutamine at amino acid position 49, using the amino acid numbering of Zhang *et al.*, supra. The terms "native" and "native sequence" OB polypeptide include the native proteins with or without the initiating N-terminal methionine (Met), and with or without the native signal sequence, either in monomeric or in dimeric form. The native human and murine OB polypeptides known in the art are 167 amino acids long, contain two conserved cysteines, and have the features of a secreted protein. The polypeptide is largely

hydrophilic, and the predicted signal sequence cleavage site is at position 21, using the amino acid numbering of Zhang *et al.*, *supra*. The overall sequence homology of the human and murine sequences is about 84%. The two proteins show a more extensive identity in the N-terminal region of the mature protein, with only four conservative and three non-conservative substitutions among the residues between the signal sequence cleavage site and the conserved Cys at position 117. The molecular weight of OB proteins is about 16 kD in a monomeric form.

A "functional derivative" of a native polypeptide is a compound having a qualitative biological property in common with the native polypeptide. A functional derivative of an OB polypeptide is a compound that has a qualitative biological property in common with a native (human or non-human) OB polypeptide. "Functional derivatives" include, but are not limited to, fragments of native polypeptides from any animal species (including humans), and derivatives of native (human and non-human) polypeptides and their fragments, provided that they have a biological activity in common with a corresponding native polypeptide.

"Fragments" comprise regions within the sequence of a mature native OB polypeptide. Preferred fragments of OB polypeptides include the C-terminus of the mature protein, and may contain relatively short deletion(s) at the N-terminus and in other parts of the molecule not required for receptor binding and/or for structural integrity.

The term "derivative" is used to define amino acid sequence variants, and covalent modifications of a native polypeptide, whereas the term "variant" refers to amino acid sequence variants within this definition.

"Biological property" in the context of the definition of "functional derivatives" is defined as either 1) immunological cross-reactivity with at least one epitope of a native polypeptide (e.g. a native OB polypeptide of any species), or 2) the possession of at least one adhesive, regulatory or effector function qualitatively in common with a native polypeptide.

Preferably, the functional derivatives are polypeptides which have at least about 65% amino acid sequence identity, more preferably about 75% amino acid sequence identity, even more preferably at least about 85% amino acid sequence identity, most preferably at least about 95% amino acid sequence identity with a native polypeptide. In the context of the present invention, functional derivatives of native sequence human OB polypeptides preferably show at least 95% amino acid sequence identity with the native OB proteins, and are not immunogenic in the human.

Amino acid sequence identity or homology is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues of a corresponding native polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity. Neither N- or C-terminal extensions nor insertions shall be construed as reducing identity or homology.

Immunologically cross-reactive as used herein means that the candidate (poly)peptide is capable of competitively inhibiting the qualitative biological activity of a corresponding native polypeptide having this activity with polyclonal antibodies or antisera raised against the known active molecule. Such antibodies and antisera are prepared in conventional fashion by injecting an animal such as a goat or rabbit, for example,

subcutaneously with the known native OB protein in complete Freud's adjuvant, followed by booster intraperitoneal or subcutaneous injection in incomplete Freud's.

The term "isolated OB polypeptide" and grammatical variants thereof refer to OB polypeptides (as hereinabove defined) separated from contaminant polypeptides present in the human, other animal species, or
5 in other source from which the polypeptide is isolated.

In general, the term "amino acid sequence variant" refers to molecules with some differences in their amino acid sequences as compared to a reference (e.g. native sequence) polypeptide. The amino acid alterations may be substitutions, insertions, deletions or any desired combinations of such changes in a native amino acid sequence.

10 Substitutional variants are those that have at least one amino acid residue in a native sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule.

Insertional variants are those with one or more amino acids inserted immediately adjacent to an amino
15 acid at a particular position in a native amino acid sequence. Immediately adjacent to an amino acid means connected to either the α -carboxy or α -amino functional group of the amino acid.

Deletional variants are those with one or more amino acids in the native amino acid sequence removed. Ordinarily, deletional variants will have one or two amino acids deleted in a particular region of the molecule.

"Covalent derivatives" include modifications of a native polypeptide or a fragment thereof with an
20 organic proteinaceous or non-proteinaceous derivatizing agent, and post-translational modifications. Covalent modifications are traditionally introduced by reacting targeted amino acid residues with an organic derivatizing agent that is capable of reacting with selected sites or terminal residues, or by harnessing mechanisms of post-translational modifications that function in selected recombinant host cells. Certain post-translational modifications are the result of the action of recombinant host cells on the expressed polypeptide. Glutaminyl
25 and asparaginyl residues are frequently post-translationally deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues may be present in the OB-immunoglobulin chimeras of the present invention. Other post-translational modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, tyrosine or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side
30 chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)].

The terms "DNA sequence encoding", "DNA encoding" and "nucleic acid encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along the polypeptide chain. The DNA sequence thus
35 codes for the amino acid sequence.

The terms "replicable expression vector" and "expression vector" refer to a piece of DNA, usually double-stranded, which may have inserted into it a piece of foreign DNA. Foreign DNA is defined as heterologous DNA, which is DNA not naturally found in the host cell. The vector is used to transport the

foreign or heterologous DNA into a suitable host cell. Once in the host cell, the vector can replicate independently of the host chromosomal DNA, and several copies of the vector and its inserted (foreign) DNA may be generated. In addition, the vector contains the necessary elements that permit translating the foreign DNA into a polypeptide. Many molecules of the polypeptide encoded by the foreign DNA can thus be rapidly synthesized.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, a ribosome binding site, and possibly, other as yet poorly understood sequences. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancer.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or a secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, then synthetic oligonucleotide adaptors or linkers are used in accord with conventional practice.

In the context of the present invention the expressions "cell", "cell line", and "cell culture" are used interchangeably, and all such designations include progeny. Thus, the words "transformants" and "transformed (host) cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same function or biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

Native immunoglobulins are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light and heavy chain variable domains (Clothia *et al.*, *J. Mol. Biol.* **186**, 651-663 (1985); Novotny and Haber, *Proc. Natl. Acad. Sci. USA* **82**, 4592-4596 [1985]).

Depending on the amino acid sequence of the constant region of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and

IgM, and several of these may be further divided into subclasses (isotypes), e.g. IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant regions that correspond to the different classes of immunoglobulins are called α , delta, epsilon, γ , and μ , respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known. IgA-1 and IgA-2 are monomeric subclasses of IgA, which usually is in the form of dimers or larger polymers. Immunocytes in the gut produce mainly polymeric IgA (also referred to poly-IgA including dimers and higher polymers). Such poly-IgA contains a disulfide-linked polypeptide called the "joining" or "J" chain, and can be transported through the glandular epithelium together with the J-containing polymeric IgM (poly-IgM), comprising five subunits.

Hybridization is preferably performed under "stringent conditions" which means (1) employing low ionic strength and high temperature for washing, for example, 0.015 sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C, or (2) employing during hybridization a denaturing agent, such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C. Another example is use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6/8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μ g/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

B. OB protein-immunoglobulin chimeras (immunoadhesins)

Immunoadhesins are chimeric antibody-like molecules that combine the functional domain(s) of a binding protein (usually a receptor, a cell-adhesion molecule or a ligand) with the an immunoglobulin sequence. The most common example of this type of fusion protein combines the hinge and Fc regions of an immunoglobulin (Ig) with domains of a cell-surface receptor that recognizes a specific ligand. This type of molecule is called an "immunoadhesin", because it combines "immune" and "adhesion" functions; other frequently used names are "Ig-chimera", "Ig-" or "Fc-fusion protein", or "receptor-globulin."

To date, more than fifty immunoadhesins have been reported in the art. Immunoadhesins reported in the literature include, for example, fusions of the T cell receptor (Gascoigne *et al.*, Proc. Natl. Acad. Sci. USA **84**, 2936-2940 [1987]); CD4 (Capon *et al.*, Nature **337**, 525-531 [1989]; Traunecker *et al.*, Nature **339**, 68-70 [1989]; Zettmeissl *et al.*, DNA Cell Biol. USA **9**, 347-353 [1990]; Byrn *et al.*, Nature **344**, 667-670 [1990]); L-selectin (homing receptor) (Watson *et al.*, J. Cell. Biol. **110**, 2221-2229 [1990]; Watson *et al.*, Nature **349**, 164-167 [1991]); E-selectin (Mulligan *et al.*, J. Immunol. **151**, 6410-17 [1993]; Jacob *et al.*, Biochemistry **34**, 1210-1217 [1995]); P-selectin (Mulligan *et al.*, *supra*; Hollenbaugh *et al.*, Biochemistry **34**, 5678-84 [1995]); ICAM-1 (Stauton *et al.*, J. Exp. Med. **176**, 1471-1476 [1992]; Martin *et al.*, J. Virol. **67**, 3561-68 [1993]; Roep *et al.*, Lancet **343**, 1590-93 [1994]); ICAM-2 (Damle *et al.*, J. Immunol. **148**, 665-71 [1992]); ICAM-3 (Holness *et al.*, J. Biol. Chem. **270**, 877-84 [1995]); LFA-3 (Kanner *et al.*, J. Immunol. **148**, 2-23-29 [1992]); L1 glycoprotein (Doherty *et al.*, Neuron **14**, 57-66 [1995]); TNF-R1 (Ashkenazi *et al.*, Proc. Natl. Acad. Sci. USA **88**, 10535-539 [1991]; Lesslauer *et al.*, Eur. J. Immunol. **21**, 2883-86 [1991]; Peppel *et al.*, J. Exp. Med. **174**, 1483-1489 [1991]); TNF-R2 (Zack *et al.*, Proc. Natl. Acad. Sci. USA **90**, 2335-39 [1993]; Wooley *et al.*, J.

Immunol. **151**, 6602-07 [1993]); CD44 [Aruffo *et al.*, *Cell* **61**, 1303-1313 (1990)]; CD28 and B7 [Linsley *et al.*, *J. Exp. Med.* **173**, 721-730 (1991)]; CTLA-4 [Lisley *et al.*, *J. Exp. Med.* **174**, 561-569 (1991)]; CD22 [Stamenkovic *et al.*, *Cell* **66**, 1133-1144 (1991)]; NP receptors [Bennett *et al.*, *J. Biol. Chem.* **266**, 23060-23067 (1991)]; IgE receptor α [Ridgway and Gorman, *J. Cell. Biol.* **115**, abstr. 1448 (1991)]; HGF receptor [Mark, M.R. *et al.*, 1992, *J. Biol. Chem.*, submitted]; IFN- γ α - and β -chain [Marsters *et al.*, *Proc. Natl. Acad. Sci. USA* **92**, 5401-05 [1995)]; trk-A, -B, and -C [Shelton *et al.*, *J. Neurosci.* **15**, 477-91 [1995)]; IL-2 (Landolfi, *J. Immunol.* **146**, 915-19 [1991]); IL-10 (Zheng *et al.*, *J. Immunol.* **154**, 5590-5600 [1995]).

The simplest and most straightforward immunoadhesin design combines the binding region(s) of the 'adhesin' protein with the hinge and Fc regions of an immunoglobulin heavy chain. Ordinarily, when preparing the OB-immunoglobulin chimeras of the present invention, nucleic acid encoding the desired OB polypeptide will be fused C-terminally to nucleic acid encoding the N-terminus of an immunoglobulin constant domain sequence, however N-terminal fusions are also possible. Typically, in such fusions the encoded chimeric polypeptide will retain at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain. Fusions are also made to the C-terminus of the Fc portion of a constant domain, or immediately N-terminal to the CH1 of the heavy chain or the corresponding region of the light chain. The precise site at which the fusion is made is not critical; particular sites are well known and may be selected in order to optimize the biological activity, secretion or binding characteristics of the OB-immunoglobulin chimeras.

In a preferred embodiment, the sequence of a native, mature OB polypeptide, is fused to the N-terminus of the C-terminal portion of an antibody (in particular the Fc domain), containing the effector functions of an immunoglobulin, e.g. IgG-1. It is possible to fuse the entire heavy chain constant region to the OB sequence. However, more preferably, a sequence beginning in the hinge region just upstream of the papain cleavage site (which defines IgG Fc chemically; residue 216, taking the first residue of heavy chain constant region to be 114 [Kobet *et al.*, *supra*], or analogous sites of other immunoglobulins) is used in the fusion. In a particularly preferred embodiment, the OB polypeptide sequence is fused to the hinge region and CH2 and CH3 or CH1, hinge, CH2 and CH3 domains of an IgG-1, IgG-2, or IgG-3 heavy chain. The precise site at which the fusion is made is not critical, and the optimal site can be determined by routine experimentation.

In some embodiments, the OB-immunoglobulin chimeras are assembled as multimers, and particularly as homo-dimers or -tetramers (WO 91/08298). Generally, these assembled immunoglobulins will have known unit structures. A basic four chain structural unit is the form in which IgG, IgD, and IgE exist. A four unit is repeated in the higher molecular weight immunoglobulins; IgM generally exists as a pentamer of basic four units held together by disulfide bonds. IgA globulin, and occasionally IgG globulin, may also exist in multimeric form in serum. In the case of multimer, each four unit may be the same or different.

Various exemplary assembled OB-immunoglobulin chimeras within the scope herein are schematically diagrammed below:

- (a) AC_L-AC_L ;
- (b) $AC_H-[AC_H, AC_L-AC_H, AC_L-V_HCH, \text{ or } V_LCL-AC_H]$;
- (c) $AC_L-AC_H-[AC_L-AC_H, AC_L-V_HCH, V_LCL-AC_H, \text{ or } V_LCL-V_HCH]$;

(d) $AC_L-V_HC_H-[AC_H, \text{ or } AC_L-V_HC_H, \text{ or } V_LC_L-AC_H]$;

(e) $V_LC_L-AC_H-[AC_L-V_HC_H, \text{ or } V_LC_L-AC_H]$; and

(f) $[A-Y]_n-[V_LC_L-V_HC_H]_2$,

wherein

5 each A represents identical or different OB polypeptide amino acid sequences;

V_L is an immunoglobulin light chain variable domain;

V_H is an immunoglobulin heavy chain variable domain;

C_L is an immunoglobulin light chain constant domain;

C_H is an immunoglobulin heavy chain constant domain;

10 n is an integer greater than 1;

Y designates the residue of a covalent cross-linking agent.

In the interests of brevity, the foregoing structures only show key features; they do not indicate joining (J) or other domains of the immunoglobulins, nor are disulfide bonds shown. However, where such domains are required for binding activity, they shall be constructed as being present in the ordinary locations which they occupy in the immunoglobulin molecules.

Alternatively, the OB amino acid sequences can be inserted between immunoglobulin heavy chain and light chain sequences such that an immunoglobulin comprising a chimeric heavy chain is obtained. In this embodiment, the OB polypeptide sequences are fused to the 3' end of an immunoglobulin heavy chain in each arm of an immunoglobulin, either between the hinge and the CH2 domain, or between the CH2 and CH3 domains. Similar constructs have been reported by Hoogenboom, H. R. *et al.*, Mol. Immunol. 28, 1027-1037 (1991).

Although the presence of an immunoglobulin light chain is not required in the immunoadhesins of the present invention, an immunoglobulin light chain might be present either covalently associated to an OB protein-immunoglobulin heavy chain fusion polypeptide, or directly fused to the OB polypeptide. In the former case, DNA encoding an immunoglobulin light chain is typically coexpressed with the DNA encoding the OB-immunoglobulin heavy chain fusion protein. Upon secretion, the hybrid heavy chain and the light chain will be covalently associated to provide an immunoglobulin-like structure comprising two disulfide-linked immunoglobulin heavy chain-light chain pairs. Method suitable for the preparation of such structures are, for example, disclosed in U.S. Patent No. 4,816,567 issued 28 March 1989.

30 In a preferred embodiment, the immunoglobulin sequences used in the construction of the immunoadhesins of the present invention are from an IgG immunoglobulin heavy chain constant domain. For human immunoadhesins, the use of human IgG-1 and IgG-3 immunoglobulin sequences is preferred. A major advantage of using IgG-1 is that IgG-1 immunoadhesins can be purified efficiently on immobilized protein A. In contrast, purification of IgG-3 requires protein G, a significantly less versatile medium. However, other structural and functional properties of immunoglobulins should be considered when choosing the Ig fusion partner for a particular immunoadhesin construction. For example, the IgG-3 hinge is longer and more flexible, so it can accommodate larger 'adhesin' domains that may not fold or function properly when fused to IgG-1. Possible IgG-based immunoadhesin structures are shown in Fig. 3a-c. While IgG immunoadhesins are typically

mono- or bivalent, other Ig subtypes like IgA and IgM may give rise to dimeric or pentameric structures, respectively, of the basic Ig homodimer unit. A typical IgM-based multimeric immunoadhesin is illustrated in Figure 3d. Multimeric immunoadhesins are advantageous in that they can bind their respective targets with greater avidity than their IgG-based counterparts. Reported examples of such structures are CD4-IgM (Traunecker *et al.*, *supra*); ICAM-IgM (Martin *et al.*, *J. Virol.* **67**, 3561-68 [1993]); and CD2-IgM (Arulanandam *et al.*, *J. Exp. Med.* **177**, 1439-50 [1993]).

For OB-Ig immunoadhesins, which are designed for *in vivo* application, the pharmacokinetic properties and the effector functions specified by the Fc region are important as well. Although IgG-1, IgG-2 and IgG-4 all have *in vivo* half-lives of 21 days, their relative potencies at activating the complement system are different. IgG-4 does not activate complement, and IgG-2 is significantly weaker at complement activation than IgG-1. Moreover, unlike IgG-1, IgG-2 does not bind to Fc receptors on mononuclear cells or neutrophils. While IgG-3 is optimal for complement activation, its *in vivo* half-life is approximately one third of the other IgG isotypes. Another important consideration for immunoadhesins designed to be used as human therapeutics is the number of allotypic variants of the particular isotype. In general, IgG isotypes with fewer serologically-defined allotypes are preferred. For example, IgG-1 has only four serologically-defined allotypic sites, two of which (G1m and 2) are located in the Fc region; and one of these sites G1m1, is non-immunogenic. In contrast, there are 12 serologically-defined allotypes in IgG-3, all of which are in the Fc region; only three of these sites (G3m5, 11 and 21) have one allotype which is nonimmunogenic. Thus, the potential immunogenicity of a γ 3 immunoadhesin is greater than that of a γ 1 immunoadhesin.

In designing the OB-Ig immunoadhesins of the present invention regions that are not required for receptor binding, the structural integrity (e.g. proper folding) and/or biological activity of the molecule, may be deleted. In such structures, it is important to place the fusion junction at residues that are located between domains, to avoid misfolding. With respect to the parental immunoglobulin, a useful joining point is just upstream of the cysteines of the hinge that form the disulfide bonds between the two heavy chains. In a frequently used design, the codon for the C-terminal residue of the "adhesin" (OB) part of the molecule is placed directly upstream of the codons for the sequence DKHTHTCPPCP of the IgG1 hinge region.

OB-Ig immunoadhesins are most conveniently constructed by fusing the cDNA sequence encoding the OB portion in-frame to an Ig cDNA sequence. However, fusion to genomic Ig fragments can also be used (see, e.g. Gascoigne *et al.*, *Proc. Natl. Acad. Sci. USA* **84**, 2936-2940 [1987]; Aruffo *et al.*, *Cell* **61**, 1303-1313 [1990]; Stamenkovic *et al.*, *Cell* **66**, 1133-1144 [1991]). The latter type of fusion requires the presence of Ig regulatory sequences for expression. cDNAs encoding IgG heavy-chain constant regions can be isolated based on published sequence from cDNA libraries derived from spleen or peripheral blood lymphocytes, by hybridization or by polymerase chain reaction (PCR) techniques. Murine OB cDNA can, for example, be obtained by PCR from a mouse adipose tissue cDNA library (Clontech), using primers designed based on the sequence of Zhang *et al.* Human OB cDNA can be obtained in a similar manner. Alternatively, the mouse OB gene can be used as a probe to isolate human adipose tissue cDNA clones (Clontech), e.g. from a λ gt11 library, as described by Zhang *et al.* The cDNAs encoding the 'adhesin' and the Ig parts of the immunoadhesin are inserted in tandem into a plasmid vector that directs efficient expression in the chosen host cells. For

expression in mammalian cells pRK5-based vectors (Schall *et al.*, Cell **61**, 361-370 [1990]), pRK7-vectors and CDM8-based vectors (Seed, Nature **329**, 840 [1989]) are preferred. (pRK7 is identical to pRK5 except that the order of the endonuclease restriction sites in the polylinker region between ClaI and HindIII is reversed. See U.S. Patent No. 5,108,901 issued 28 April 1992.). The exact junction can be created by removing the extra sequences between the designed junction codons using oligonucleotide-directed deletional mutagenesis (Zoller and Smith, Nucleic Acids Res. **10**, 6487 [1982]; Capon *et al.*, Nature **337**, 525-531 [1989]). Synthetic oligonucleotides can be used, in which each half is complementary to the sequence on either side of the desired junction; ideally, these are 36 to 48-mers. Alternatively, PCR technique can be used to join the two parts of the molecule in-frame with an appropriate vector.

Immunoadhesins can be expressed efficiently in a variety of host cells, including myeloma cell lines, Chinese Hamster ovary (CHO) cells, monkey COS cells, human embryonic kidney 293 cells, and baculovirus infected insect cells. In these systems, the immunoadhesin polypeptides are assembled and secreted into the cell culture medium. Yeasts, e.g. Saccharomyces cerevisiae, Pichia pastoris, etc., and bacterial cells, preferably E. coli, can also be used as hosts. The OB-immunoglobulin chimeras can be expressed in yeast, for example, similarly to the process described for the expression of the OB proteins by Leiber *et al.*, Crit. Res. Food Sci. Nutr. **33**, 351 (1993); Friedman and Leibel, Cell **69**, 217 (1992); and Beavis and Chait, Proc. Natl. Acad. Sci. USA **87**, 6873 (1990). Thus, the coding sequences can be subcloned into a yeast plasmid, such as the yeast expression plasmid pPIC.9 (Invitrogen). This vector directs secretion of heterologous proteins from the yeast into the culture media. According to Halaas *et al.*, *supra*, expression of mouse and human OB genes in Saccharomyces cerevisiae transformed with this vector yields a secreted 16-kD protein, which is an unprocessed OB protein lacking the signal sequence. Expression of the mouse or human OB-immunoglobulin chimeras in E. coli can, for example, be performed on the analogy of the procedure described by Halaas *et al.*, *supra*. The coding sequences of mouse and human OB-immunoglobulin chimeras can be subcloned into the PET15b expression vector (Novagen) and expressed in E. coli (BL21 (DE3)pIYsS) through use of the T7 E. coli RNA polymerase system. Alternatively, the fusion protein can be expressed in E. coli by inserting the coding sequence in frame with the secretion sequence of the E. coli heat stable enterotoxin II, downstream of the E. coli alkaline phosphatase promoter (Chang *et al.*, Gene **55**, 189-96 [1987]).

The choice of host cell line for the expression of OB-Ig immunoadhesins depends mainly on the expression vector. Another consideration is the amount of protein that is required. Milligram quantities often can be produced by transient transfections. For example, the adenovirus EIA-transformed 293 human embryonic kidney cell line can be transfected transiently with pRK5- and pRK7-based vectors by a modification of the calcium phosphate method to allow efficient immunoadhesin expression. This method is illustrated in the examples. CDM8-based vectors can be used to transfect COS cells by the DEAE-dextran method (Aruffo *et al.*, Cell **61**, 1303-1313 (1990); Zettmeissl *et al.*, DNA Cell Biol. (US) **9**, 347-353 (1990)). If larger amounts of protein are desired, the immunoadhesin can be expressed after stable transfection of a host cell line. For example, a pRK5- or pRK7-based vector can be introduced into Chinese hamster ovary (CHO) cells in the presence of an additional plasmid encoding dihydrofolate reductase (DHFR) and conferring resistance to G418. Clones resistant to G418 can be selected in culture; these clones are grown in the presence of increasing levels

of DHFR inhibitor methotrexate; clones are selected, in which the number of gene copies encoding the DHFR and immunoadhesin sequences is co-amplified. If the immunoadhesin contains a hydrophobic leader sequence at its N-terminus, it is likely to be processed and secreted by the transfected cells. The expression of immunoadhesins with more complex structures may require uniquely suited host cells; for example, components such as light chain or J chain may be provided by certain myeloma or hybridoma cell hosts [Gascoigne *et al.*, 5 1987, *supra*; Martin *et al.*, *J. Virol.* **67**, 3561-3568 (1993)].

The expression of immunoadhesins with more complex oligomeric structures may require uniquely suited host cells; for example, components such as light chain or J chain may be provided by certain myeloma or hybridoma cell hosts (Gascoigne *et al.*, *supra*; Martin *et al.*, *J. Immunol.* **67**, 3561-68 [1993]).

10 Immunoadhesins can be conveniently purified by affinity chromatography. The suitability of protein A as an affinity ligand depends on the species and isotype of the immunoglobulin Fc domain that is used in the chimera. Protein A can be used to purify immunoadhesins that are based on human $\gamma 1$, $\gamma 2$, or $\gamma 4$ heavy chains [Lindmark *et al.*, *J. Immunol. Meth.* **62**, 1-13 (1983)]. Protein G is recommended for all mouse isotypes and for human $\gamma 3$ [Guss *et al.*, *EMBO J.* **5**, 1567-1575 (1986)]. The matrix to which the affinity ligand is attached 15 is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrene-divinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. The conditions for binding an immunoadhesin to the protein A or G affinity column are dictated entirely by the characteristics of the Fc domain; that is, its species and isotype. Generally, when the proper ligand is chosen, efficient binding occurs directly from unconditioned culture fluid. One distinguishing 20 feature of immunoadhesins is that, for human $\gamma 1$ molecules, the binding capacity for protein A is somewhat diminished relative to an antibody of the same Fc type. Bound immunoadhesin can be efficiently eluted either at acidic pH (at or above 3.0), or in a neutral pH buffer containing a mildly chaotropic salt. This affinity chromatography step can result in an immunoadhesin preparation that is >95% pure.

Other methods known in the art can be used in place of, or in addition to, affinity chromatography on 25 protein A or G to purify immunoadhesins. Immunoadhesins behave similarly to antibodies in thiophilic gel chromatography [Hutchens and Porath, *Anal. Biochem.* **159**, 217-226 (1986)] and immobilized metal chelate chromatography [Al-Mashikhi and Makai, *J. Dairy Sci.* **71**, 1756-1763 (1988)]. In contrast to antibodies, however, their behavior on ion exchange columns is dictated not only by their isoelectric points, but also by a charge dipole that may exist in the molecules due to their chimeric nature. Microheterogeneity of charge can 30 also be a factor for immunoadhesins in which the adhesin portion of the molecule is glycosylated and contains sialic acid. A specific purification protocol is described in the examples.

Results with the numerous immunoadhesins produced so far show that the fusion of the adhesin portion to an Fc region usually does not perturb the folding of the individual domains. Both the adhesin and the immunoglobulin regions appear to fold correctly, and the Fc portion retains many of the effector functions that 35 are characteristic of antibodies, such as binding to Fc receptors.

Methods generally applicable for the construction, expression and purification of immunoadhesins are described, for example, in U.S. Patent Nos. 5,225,538 (issued 6 July 1993) and 5,455,165 (issued 30 October 1995), the disclosures of which are hereby expressly incorporated by reference. Immunoadhesin construction,

expression, purification and various immunoadhesins designs are also described in the review articles by Ashkenazi and Chamow, Methods in Enzymology 8, 104-115 (1995), and Peach and Linsley, Methods in Enzymology 8, 116-123 (1995), the disclosures of which, along with the references cited therein, is hereby expressly incorporated by reference.

5 C. Other long half-life OB derivatives

Other derivatives of the OB proteins, which possess a longer half-life than the native molecules comprise the OB protein or an OB-immunoglobulin chimera, covalently bonded to a nonproteinaceous polymer. The nonproteinaceous polymer ordinarily is a hydrophilic synthetic polymer, i.e., a polymer not otherwise found in nature. However, polymers which exist in nature and are produced by recombinant or *in vitro* methods are
10 useful, as are polymers which are isolated from native sources. Hydrophilic polyvinyl polymers fall within the scope of this invention, e.g. polyvinylalcohol and polyvinylpyrrolidone. Particularly useful are polyalkylene ethers such as polyethyleneglycol (PEG); polyalkylenes such as polyoxyethylene, polyoxypropylene, and block copolymers of polyoxyethylene and polyoxypropylene (Pluronics); polymethacrylates; carbomers; branched or unbranched polysaccharides which comprise the saccharide monomers D-mannose, D- and L-galactose,
15 fucose, fructose, D-xylose, L-arabinose, D-glucuronic acid, sialic acid, D-galacturonic acid, D-mannuronic acid (e.g. polymannuronic acid, or alginic acid), D-glucosamine, D-galactosamine, D-glucose and neuraminic acid including homopolysaccharides and heteropolysaccharides such as lactose, amylopectin, starch, hydroxyethyl starch, amylose, dextran sulfate, dextran, dextrans, glycogen, or the polysaccharide subunit of acid mucopolysaccharides, e.g. hyaluronic acid; polymers of sugar alcohols such as polysorbitol and polymannitol;
20 heparin or heparan. The polymer prior to cross-linking need not be, but preferably is, water soluble, but the final conjugate must be water soluble. In addition, the polymer should not be highly immunogenic in the conjugate form, nor should it possess viscosity that is incompatible with intravenous infusion or injection if it is intended to be administered by such routes.

Preferably the polymer contains only a single group which is reactive. This helps to avoid cross-linking
25 of protein molecules. However, it is within the scope herein to optimize reaction conditions to reduce cross-linking, or to purify the reaction products through gel filtration or chromatographic sieves to recover substantially homogenous derivatives.

The molecular weight of the polymer may desirably range from about 100 to 500,000, and preferably is from about 1,000 to 20,000. The molecular weight chosen will depend upon the nature of the polymer and
30 the degree of substitution. In general, the greater the hydrophilicity of the polymer and the greater the degree of substitution, the lower the molecular weight that can be employed. Optimal molecular weights will be determined by routine experimentation.

The polymer generally is covalently linked to the OB protein or to the OB-immunoglobulin chimeras through a multifunctional crosslinking agent which reacts with the polymer and one or more amino acid or sugar
35 residues of the OB protein or OB-immunoglobulin chimera to be linked. However, it is within the scope of the invention to directly crosslink the polymer by reacting a derivatized polymer with the hybrid, or via versa.

The covalent crosslinking site on the OB protein or OB-Ig includes the N-terminal amino group and epsilon amino groups found on lysine residues, as well as other amino, imino, carboxyl, sulfhydryl, hydroxyl or other hydrophilic groups. The polymer may be covalently bonded directly to the hybrid without the use of a multifunctional (ordinarily bifunctional) crosslinking agent. Covalent binding to amino groups is accomplished by known chemistries based upon cyanuric chloride, carbonyl diimidazole, aldehyde reactive groups (PEG alkoxide plus diethyl acetal of bromoacetaldehyde; PEG plus DMSO and acetic anhydride, or PEG chloride plus the phenoxide of 4-hydroxybenzaldehyde, succinimidyl active esters, activated dithiocarbonate PEG, 2,4,5-trichlorophenylchloroformate or P-nitrophenylchloroformate activated PEG.) Carboxyl groups are derivatized by coupling PEG-amine using carbodiimide.

Polymers are conjugated to oligosaccharide groups by oxidation using chemicals, e.g. metaperiodate, or enzymes, e.g. glucose or galactose oxidase, (either of which produces the aldehyde derivative of the carbohydrate), followed by reaction with hydrazide or amino derivatized polymers, in the same fashion as is described by Heitzmann *et al.*, P.N.A.S., 71, 3537-41 (1974) or Bayer *et al.*, Methods in Enzymology 62, 310 (1979), for the labeling of oligosaccharides with biotin or avidin. Further, other chemical or enzymatic methods which have been used heretofore to link oligosaccharides are particularly advantageous because, in general, there are fewer substitution sites than amino acid sites for derivatization, and the oligosaccharide products thus will be more homogenous. The oligosaccharide substituents also are optionally modified by enzyme digestion to remove sugars, e.g. by neuraminidase digestion, prior to polymer derivatization.

The polymer will bear a group which is directly reactive with an amino acid side chain, or the N- or C-terminus of the polypeptide linked, or which is reactive with the multifunctional cross-linking agent. In general, polymers bearing such reactive groups are known for the preparation of immobilized proteins. In order to use such chemistries here, one should employ a water soluble polymer otherwise derivatized in the same fashion as insoluble polymers heretofore employed for protein immobilization. Cyanogen bromide activation is a particularly useful procedure to employ in crosslinking polysaccharides.

"Water soluble" in reference to the starting polymer means that the polymer or its reactive intermediate used for conjugation is sufficiently water soluble to participate in a derivatization reaction.

"Water soluble" in reference to the polymer conjugate means that the conjugate is soluble in physiological fluids such as blood.

The degree of substitution with such a polymer will vary depending upon the number of reactive sites on the protein, whether all or a fragment of the protein is used, whether the protein is a fusion with a heterologous protein (e.g. an OB-immunoglobulin chimera), the molecular weight, hydrophilicity and other characteristics of the polymer, and the particular protein derivatization sites chosen. In general, the conjugate contains about from 1 to 10 polymer molecules, while any heterologous sequence may be substituted with an essentially unlimited number of polymer molecules so long as the desired activity is not significantly adversely affected. The optimal degree of cross-linking is easily determined by an experimental matrix in which the time, temperature and other reaction conditions are varied to change the degree of substitution, after which the ability of the conjugates to function in the desired fashion is determined.

The polymer, e.g. PEG, is cross-linked by a wide variety of methods known *per se* for the covalent modification of proteins with nonproteinaceous polymers such as PEG. Certain of these methods, however, are not preferred for the purposes herein. Cyanuronic chloride chemistry leads to many side reactions, including protein cross-linking. In addition, it may be particularly likely to lead to inactivation of proteins containing 5 sulfhydryl groups. Carbonyl diimidazole chemistry (Beauchamp *et al.*, Anal. Biochem. 131, 25-33 [1983]) requires high pH (>8.5), which can inactivate proteins. Moreover, since the "activated PEG" intermediate can react with water, a very large molar excess of "activated PEG" over protein is required. The high concentrations of PEG required for the carbonyl diimidazole chemistry also led to problems in purification, as both gel filtration chromatography and hydrophilic interaction chromatography are adversely affected. In addition, the high 10 concentrations of "activated PEG" may precipitate protein, a problem that *per se* has been noted previously (Davis, U.S. Patent No. 4,179,337). On the other hand, aldehyde chemistry (Royer, U.S. Patent No. 4,002,531) is more efficient since it requires only a 40-fold molar excess of PEG and a 1-2 hr incubation. However, the manganese dioxide suggested by Royer for preparation of the PEG aldehyde is problematic "because of the pronounced tendency of PEG to form complexes with metal-based oxidizing agents" (Harris *et al.*, J. Polym. Sci. Polym. Chem. Ed. 22, 341-52 [1984]). The use of a Moffatt oxidation, utilizing DMSO and acetic anhydride, obviates this problem. In addition, the sodium borohydride suggested by Royer must be used at high pH and has a significant tendency to reduce disulfide bonds. In contrast, sodium cyanoborohydride, which is effective at neutral pH and has very little tendency to reduce disulfide bonds is preferred.

Functionalized PEG polymers to modify the OB protein or OB-Ig chimeras of the present invention 20 are available from Shearwater Polymers, Inc. (Huntsville, AL). Such commercially available PEG derivatives include, but are not limited to, amino-PEG, PEG amino acid esters, PEG-hydrazide, PEG-thiol, PEG-succinate, carboxymethylated PEG, PEG-propionic acid, PEG amino acids, PEG succinimidylsuccinate, PEG succinimidyl propionate, succinimidylester of carboxymethylated PEG, succinimidyl carbonate of PEG, succinimidyl esters of amino acid PEGs, PEG-oxycarbonylimidazole, PEG-nitrophenyl carbonate, PEG tresylate, PEG-glycidyl 25 ether, PEG-aldehyde, PEG vinylsulfone, PEG-maleimide, PEG-orthopyridyl-disulfide, heterofunctional PEGs, PEG vinyl derivatives, PEG silanes, and PEG phospholides. The reaction conditions for coupling these PEG derivatives will vary depending on the protein, the desired degree of PEGylation, and the PEG derivative utilized. Some factors involved in the choice of PEG derivatives include: the desired point of attachment (lysine or cysteine), hydrolytic stability and reactivity of the derivatives, stability, toxicity and antigenicity of the 30 linkage, suitability for analysis, etc. Specific instructions for the use of any particular derivative are available from the manufacturer.

The long half-life conjugates of this invention are separated from the unreacted starting materials by gel filtration. Heterologous species of the conjugates are purified from one another in the same fashion. The polymer also may be water-insoluble, as a hydrophilic gel.

35 The conjugates may also be purified by ion-exchange chromatography. The chemistry of many of the electrophilically activated PEG's results in a reduction of amino group charge of the PEGylated product. Thus, high resolution ion exchange chromatography can be used to separate the free and conjugated proteins, and to resolve species with different levels of PEGylation. In fact, the resolution of different species (e.g. containing

one or two PEG residues) is also possible due to the difference in the ionic properties of the unreacted amino acids.

D. The use of the OB-immunoglobulin chimeras and other long half-life derivatives

The OB-immunoglobulin chimeras and other long half-life OB derivatives of the present invention are useful for weight reduction, and specifically, in the treatment of obesity and other disorders associated with the abnormal expression or function of the OB gene. Our studies indicate that the OB-immunoglobulin chimeras and other long half-life OB derivatives, e.g. PEGylated OB, reduce the food intake and increase the energy use of animals treated, and are therefore very effective in reducing the weight of both obese and normal subjects. For testing purposes, the molecules of the present invention may be dissolved in phosphate-buffered saline (PBS) (pH 7.4), and administered by intravenous or subcutaneous injection, or infusion.

The long acting OB-derivatives of the present invention may further be used to treat other metabolic disorders such as diabetes and bulimia. The OB protein has been shown to reduce insulin levels in animals, and could be useful to reduce excessive levels of insulin in human patients. The reduction of insulin levels in obese or non-obese patients (e.g. Type I or II diabetics) could restore or improve the insulin-sensitivity of such patients.

In addition, the long half-life OB-derivatives can be used for the treatment of kidney ailments, hypertension, and lung disfunctions, such as emphysema. The OB protein might also cause a mitogenic response in receptor-bearing tissues, acting as a growth factor for these cells.

Therapeutic formulations of the present invention are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as Tween, Pluronic or PEG.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, etc. routes. Sustained release formulations are also foreseen. Suitable examples of sustained release preparations include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices include polyesters, hydrogels, polylactides (U.S. Patent 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (U. Sidman *et al.*, 1983, "Biopolymers" **22** (1): 547-556), poly (2-hydroxyethyl-methacrylate) (R. Langer, *et al.*, 1981, "J. Biomed. Mater. Res." **15**: 167-277 and R. Langer, 1982, Chem. Tech." **12**: 98-105), ethylene vinyl acetate (R. Langer *et al.*, *Id.*) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988A). Sustained release compositions also include liposomes. Liposomes containing a molecule within the scope of the present invention are prepared by methods known *per se*: DE 3,218,121A; Epstein *et al.*, 1985, "Proc. Natl. Acad. Sci. USA" **82**: 3688-3692; Hwang *et al.*, 1980, "Proc. Natl. Acad. Sci. USA" **77**: 4030-4034; EP 52322A; EP 36676A; EP 88046A; EP 143949A; EP 142641A; Japanese patent application 83-118008; U.S. patents 4,485,045 and 4,544,545; and EP 102,324A. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. % cholesterol, the selected proportion being adjusted for the optimal therapy.

An effective amount of a molecule of the present invention to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage might range from about 1 µg/kg to up to 100 mg/kg or more, depending on the factors mentioned above. Typically, the clinician will administer a molecule of the present invention until a dosage is reached that provides the required biological effect. The progress of this therapy is easily monitored by conventional assay techniques. If the purpose of the treatment is weight reduction, the therapy is normally continued until a desired body weight is reached.

Non-therapeutic uses of the OB protein-immunoglobulin fusions of the present invention include their use to identify and purify OB receptors. The identification and expression cloning of an OB receptor, using an OB protein-immunoadhesin is described in a Reference Example hereinbelow.

The invention will be further illustrated by the following non-limiting examples.

Example 1

Expression of OB-immunoadhesins

Using protein engineering techniques, the human OB protein was expressed as a fusion with the hinge, CH2 and CH3 domains of IgG-1. DNA constructs encoding the chimera of the human OB protein and IgG-1 Fc domains were made with the Fc region clones of human IgG-1. Human OB cDNA was obtained by PCR from human fat cell cDNA (Clontech Buick-Clone cDNA product). The source of the IgG-1 cDNA was the plasmid pBSSK-CH₂CH₃. The chimera contained the coding sequence of the full length OB protein (amino acids 1-167 in Figure 5) and human IgG-1 sequences beginning at aspartic acid 216 (taking amino acid 114 as the first residue of the heavy chain constant region (Kabat *et al.*, Sequences of Proteins of Immunological

Interest 4th ed. [1987]), which is the first residue of the IgG-1 hinge after the cysteine residue involved in heavy-light chain bonding, and ending with residues 441 to include the CH2 and CH3 Fc domains of IgG-1. There was an insert of codons for three amino acids (GlyValThr) between the OB and IgG-1 coding sequences. If necessary, this short linker sequence can easily be deleted, for example by site directed deletion mutagenesis, to create an exact junction between the coding sequences of the OB protein and the IgG-1 hinge region. The coding sequence of the OB-IgG-1 immunoadhesin was subcloned into the pRK5-based vector pRK5tk-neo which contains a neomycin selectable marker, for transient expression in 293 cells using the calcium phosphate technique (Suva *et al.*, Science 237, 893-896 [1987]). 293 cells were cultured in HAM's: Low Glucose DMEM medium (50:50), containing 10% FBS and 2 mM L-Gln. For purification of OB-IgG-1 chimeras, cells were changed to serum free production medium PS24 the day after transfection and media collected after three days. The culture media was filtered.

The filtered 293 cell supernatant (400 ml) containing recombinant human OB-IgG-1 was made 1 mM in phenylmethylsulfonyl fluoride and 2 µg/ml in aprotinin. This material was loaded at 4 °C onto a 1 x 4.5 cm Protein A agarose column (Pierce catalog # 20365) equilibrated in 100 mM HEPES pH 8. The flow rate was 75 ml/h. Once the sample was loaded, the column was washed with equilibration buffer until the A₂₈₀ reached baseline. The OB-IgG-1 protein was eluted with 3.5 M MgCl₂ + 2% glycerol (unbuffered) at a flow rate of 15 ml/h. The eluate was collected with occasional mixing into 10 ml of 100 mM HEPES pH 8 to reduce the MgCl₂ concentration by approximately one-half and to raise the pH. The eluted protein was then dialyzed into phosphate buffered saline, concentrated, sterile filtered and stored either at 4 °C or frozen at -70 °C. The OB-IgG-1 immunoadhesin prepared by this method is estimated by SDS-PAGE to be greater than 90% pure.

Example 2

Animal studies

A. Materials and Methods

OB protein Production -- Murine OB cDNA was obtained by PCR from an adipocyte cDNA library using primers based on the sequence of Zhang *et al.*, *supra*. Mature OB protein (amino acids 22-167) was expressed in *E. coli* by inserting the OB coding sequence in frame with the secretion sequence of the *E. coli* heat-stable enterotoxin II, downstream of the *E. coli* alkaline phosphatase promoter. Chang *et al.*, Gene 55, 189-96 (1987). After cell lysis, the insoluble fraction was solubilized in 8 M urea buffer pH 8.35 in the presence of 25 mM DTT. Reduced OB protein was purified by size exclusion and reverse phase HPLC, then refolded in the presence of glutathione. Refolded OB protein was purified by reverse phase HPLC and analyzed by SDS-PAGE and amino acid and mass spectrometry analyses.

Preparation of PEG-hOB -- The PEG derivatives of the human PB protein were prepared by reaction of hOB purified by reverse phase chromatography with a succinimidyl derivative of PEG propionic acid (SPA-PEG) having a nominal molecular weight of 10 kD, which had been obtained from Shearwater Polymers, Inc. (Huntsville, AL). After purification of the hOB protein by reverse phase chromatography, an approximately 1-2 mg/ml solution of the protein in 0.1% trifluoroacetic acid and approximately 40% acetonitrile was diluted with 1/3 to 1/2 volume of 0.2 M borate buffer and the pH adjusted to 8.5 with NaOH. SPA-PEG was added to

the reaction mixture to make 1:1 and 1:2 molar ratios of protein to SPA-PEG and the mixture was allowed to incubate at room temperature for one hour. After reaction and purification by gel electrophoresis or ion exchange chromatography, the samples were extensively dialyzed against phosphate-buffered saline and sterilized by filtration through a 0.22 micron filter. Samples were stored at 4°C. Under these conditions, the PEG-hOB resulting from the 1:1 molar ratio protein to SPA-PEG reaction consisted primarily of molecules with one 10 kD PEG attached with minor amounts of the 2 PEG-containing species. The PEG-hOB from the 1:2 molar reaction consisted of approximately equal amounts of 2 and 3 PEGs attached to hOB, as determined by SDS gel electrophoresis. In both reactions, small amounts of unreacted protein was also detected. This unreacted protein can be efficiently removed by the gel filtration or ion exchange steps as needed. The PEG derivatives of the human OB protein can also be prepared essentially following the aldehyde chemistry described in EP 372,752 published June 13, 1990.

Animal Studies -- All manipulations involving animals were reviewed and approved by Genentech's Institutional Animal Care and Use Committee. Seven to eight week-old genetically obese C57Bl/6J-*ob/ob* (*ob/ob*) female mice were purchased from Jackson Labs (Bar Harbor, ME). Lean female mice of the same genetic background (C57Bl/6) were purchased from Harlan Sprague Dawley (Hollister, CA). Mice were housed in groups 3 - 6 with *ad libitum* access to water and standard mouse chow (Purina 5010; Purina Mills, Richmond, IN) in a temperature-, humidity- and light-controlled (lights on at 06:00h, off at 18:00h) colony room.

Miniosmotic pumps (Alzet model 2002; Alza Corp., Palo Alto, CA) were filled with purified recombinant OB protein (100 µg/kg/day) in sterile phosphate-buffered saline (PBS) or PBS alone under sterile conditions following manufacturer's instructions and incubated overnight in sterile saline at room temperature prior to implantation into mice. Mice were anesthetized with ketamine/xylazine, and miniosmotic pumps were implanted subcutaneously in the midscapular region. Daily subcutaneous injections of purified recombinant OB protein, hOB-IgG-1 fusion protein or PBS were made into the midscapular region of conscious mice. Injections were performed within one hour of lights out. The body weight of each mouse (to the nearest 0.1 gram) and the weight of the food contained in the food bin in each cage (to the nearest 0.1 gram) were recorded within one hour of lights out every one to two days. The data are depicted as the mean ± SEM. The number of animals is as described below and in the Figure legends.

B. Results with continuous subcutaneous infusion of OB protein

Lean female mice were treated with murine OB protein either as a continuous subcutaneous infusion or daily subcutaneous injections. The results are shown in Figure 1. The upper chart shows that the OB protein is significantly more effective in reducing body weight when delivered as a continuous infusion than when the same dose is delivered in the form of daily subcutaneous injections. The bottom chart shows the same difference in the ability of the OB protein to reduce adipose tissue weight.

C. Results with the OB-IgG-1 chimera

Obese female *ob/ob* mice were treated with human OB protein or with the human OB-IgG-1 chimera. The data are shown in Figure 2. The data presented in the top chart demonstrate that the hOB-IgG-1 fusion

protein is more potent than the native hOB protein at reducing body weight, when both proteins are administered similarly by daily subcutaneous infusion. It is noted that the increase in potency would be even more expressed, if the data were converted to molar amounts, as only about one third of the OB-IgG-1 chimera comes from the OB protein. The data further confirm the previous observation that continuous subcutaneous infusion (pump) or the hOB protein is more effective than daily subcutaneous injections (inj) at reducing body weight.

The data shown at the bottom chart of Figure 2 show that the hOB-IgG-1 fusion protein substantially reduced food intake. This result was unexpected as it was assumed that the fusion protein would be too large to cross the blood-brain barrier and exert its effect.

Obese (*ob/ob*) female mice were treated with either hOB or the hOB-IgG-1 chimera by daily subcutaneous injections for 7 days. The data shown in Figure 3 again demonstrate that the chimera is more effective than the native hOB protein at reducing body weight (top) and food intake (bottom).

In a further experiment, obese (*ob/ob*) female mice were treated with either the hOB-IgG-1 fusion protein, native hOB or hCD4-IgG-1 (control) by daily subcutaneous injections for seven days. The results shown in Figure 5 affirm that the hOB-IgG-1 fusion protein is more effective than the native hOB protein at reducing body weight (top and middle panels) and food intake (bottom panel).

D. Results with PEG-hOB

Obese female *ob/ob* mice were treated with human OB protein or with PEG derivatives of human OB. The data are shown in Figure 4. The data presented in the top chart demonstrate that PEG-hOB is more potent than the native hOB protein at reducing body weight, when both proteins are administered similarly by daily subcutaneous infusion.

The data shown at the bottom chart of Figure 4 show that the PEG-hOB proteins were substantially more effective in reducing food intake than unmodified native hOB.

Reference Example

Identification and cloning of an OB receptor

The OB protein-immunoadhesin of Example 1 was used to detect and expression clone an OB receptor. First, to identify a receptor source, several cell lines were screened with 1 µg/ml OB-IgG-1 fusion by flow cytometry. The detection system which consists of a biotin conjugated secondary antibody followed by streptavidin-phycoerythrin provides a dramatic amplification of the signal and allows the detection of cells expressing low numbers of receptors. Two cell lines, human embryonic kidney 293 and human lung A549 cells were found to bind OB-IgG-1 but not an Flt-4 control immunoadhesin. Specific binding of OB-IgG-1 to the cells was also demonstrated by the addition of excess of bacterially expressed human OB protein. Addition of 10 µg/ml of human OB completely blocks the binding of OB-IgG-1 to 293 cells.

To isolate a cDNA encoding the OB receptor, COSN cells were transiently transfected with pools of approximately 10⁵ clones of an oligo dT primed 293 cell cDNA library in pRK5B. Transfected cells were enriched by panning on plates coated with an anti-human Fc antibody after incubation with OB-IgG-1. After

three rounds of enrichment, 1 of 30 pools gave rise to OB-IgG-1 mediated adherence of COSN cells to the binding plates which could be competed by human leptin. cDNA clones picked randomly from this third round were transfected in pools of 10-20. Individual clones were finally identified after breaking down one pool of 10 that was scoring positive by panning.

- 5 Sequence analysis revealed a clone of approximately 5300 bp with an open reading frame encoding a protein of 896 amino acids. The sequence corresponded to a type 1 transmembrane protein with a 22 amino acid long signal peptide, 819 amino acid extracellular domain, 21 amino acid transmembrane domain and a short 34 amino acid intracellular domain. The sequence was found to essentially correspond to the human OB receptor identified and isolated by Tartaglia *et al.*, *supra*, and is identical with a human receptor sequence
- 10 disclosed in copending application Serial No. 08/585,005 filed January 11, 1996.

 While the invention has been illustrated by way of examples, the scope of the invention is not so limited. It will be understood that further modifications and variations are possible without diverting from the overall concept of the invention. All such modifications are intended to be within the scope of the present invention.

- 15 All references cited throughout the specification, including the examples, and the references cited therein are hereby expressly incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Genentech, Inc.
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- (ii) TITLE OF INVENTION: OB Protein Derivatives
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(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 19-Dec-1996
(C) CLASSIFICATION:
- 25 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/667184
(B) FILING DATE: 20-JUN-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/579494
30 (B) FILING DATE: 27-DEC-1995
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(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7127 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG 6050
CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG 6100
ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT 6150
AGGTGCCTCA CTGATTAAGC ATTGGTAACT GTCAGACCAA GTTTACTCAT 6200
15 ATATACTTTA GATTGATTTA AAACCTCATT TTTAATTTAA AAGGATCTAG 6250
GTGAAGATCC TTTTGTGATA TCTCATGACC AAAATCCCTT AACGTGAGTT 6300
TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT 6350
GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAACCA 6400
CCGCTACCAG CCGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT 6450
20 TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC 6500
TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT 6550
ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA 6600
TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG 6650
CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG 6700
25 CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC ATTGAGAAAG 6750
CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA 6800
GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG 6850
TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT 6900

TTTGTGATGC TCGTCAGGGG GCGGAGCCT ATGGA AAAAC GCCAGCTGGC 6950
 ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT 7000
 GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC 7050
 GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA 7100

5 ACAGCTATGA CCATGATTAC GAATTAA 7127

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: Amino Acid

10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	
	1				5					10					15	
15	Leu	Phe	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	
				20						25					30	
	Thr	Lys	Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	
				35						40					45	
	Ser	His	Thr	Gln	Ser	Val	Ser	Ser	Lys	Gln	Lys	Val	Thr	Gly	Leu	
				50						55					60	
20	Asp	Phe	Ile	Pro	Gly	Leu	His	Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	
				65						70					75	
	Asp	Gln	Thr	Leu	Ala	Val	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	
				80						85					90	
25	Ser	Arg	Asn	Val	Ile	Gln	Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	
				95						100					105	
	Asp	Leu	Leu	His	Val	Leu	Ala	Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	
				110						115					120	
	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	Asp	Ser	Leu	Gly	Gly	Val	Leu	
				125						130					135	
30	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	Ser	Arg	Leu	
				140						145					150	
	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	Leu	Asp	Leu	Ser	Pro	
				155						160					165	
35	Gly	Cys	Gly	Val	Thr	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
				170						175					180	
	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	

	185	190	195
	Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr		
	200	205	210
5	Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe		
	215	220	225
	Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys		
	230	235	240
	Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val		
	245	250	255
10	Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		
	260	265	270
	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
	275	280	285
15	Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr		
	290	295	300
	Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu		
	305	310	315
	Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
	320	325	330
20	Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
	335	340	345
	Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu		
	350	355	360
25	Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
	365	370	375
	Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser		
	380	385	390
	Leu Ser Leu Ser Pro Gly Lys		
	395	397	

CLAIMS:

1. A long half-life derivative of an OB protein retaining a biological property of a native OB protein.
2. The long half-life derivative of claim 1 capable of reducing body weight and/or food
5 intake in an individual treated.
3. The derivative of claim 1 which is a derivative of a native human OB protein.
4. The derivative of claim 1 which is an OB-immunoglobulin chimera.
5. The derivative of claim 1 which is a native OB protein or an OB-immunoglobulin chimera
modified with a nonproteinaceous polymer.
- 10 6. The derivative of claim 4 wherein the nonproteinaceous polymer is polyethylene glycol (PEG).
7. A composition for the treatment of a condition associated with the abnormal expression or function of the OB gene, or for eliciting a biological response mediated by an OB receptor, comprising an effective amount of an OB derivative of claim 1.
- 15 8. The composition of claim 7 effective for weight and/or appetite reduction.
9. The composition of claim 7 effective in the reduction of elevated insulin levels.
10. A method for the treatment of a condition associated with the abnormal expression or function of the OB gene, or for eliciting a biological response mediated by an OB receptor, comprising administering to an individual to be treated a derivative of claim 1.
- 20 11. The method of claim 10 wherein the condition to be treated is selected from the group consisting of obesity, bulimia, and Type I or II diabetes.
12. A method for inducing weight loss or appetite loss in a subject, comprising administering to said subject an effective amount of a derivative of claim 1.
13. A chimeric polypeptide comprising an OB protein amino acid sequence capable of
25 binding to a native OB receptor, linked to an immunoglobulin sequence.
14. The chimeric polypeptide of claim 13 wherein said immunoglobulin sequence is a constant domain sequence.
15. The chimeric polypeptide of claim 14 wherein said OB protein is human.
16. The chimeric polypeptide of claim 15 wherein two OB polypeptide-IgG heavy chain
30 fusions are linked to each other by at least one disulfide bond to yield a homodimeric immunoglobulin-like structure.
17. The chimeric polypeptide of claim 16 wherein at least one of said OB polypeptide-IgG heavy chain fusions is associated with an immunoglobulin light chain.
18. An isolated nucleic acid sequence encoding an OB protein-immunoglobulin fusion.
- 35 19. A replicable expression vector comprising the nucleic acid of claim 18.
20. A host cell transformed with the replicable expression vector of claim 19.
21. A process comprising culturing the host cells of claim 16 so as to express the nucleic acid encoding an OB protein-immunoglobulin fusion.

22. The process of claim 21 wherein said host cells are cotransformed with nucleic acid encoding at least two OB protein-immunoglobulin fusions.

23. The process of claim 22 wherein said cells are further transformed with nucleic acid encoding at least one immunoglobulin light chain.

5 24. A method of treating a condition associated with the abnormal expression or function of the OB gene or for eliciting a biological response mediated by an OB receptor comprising administering to a patient a therapeutically effective amount of the chimeric polypeptide of claim 13.

25. The method of claim 20 wherein said condition is selected from the group consisting of obesity, bulimia and type I or II diabetes.

10 26. A composition for the treatment of obesity comprising an effective amount of a chimeric polypeptide of claim 13 in association with a pharmaceutically acceptable carrier.

27. A method for inducing the growth of cells expressing an OB receptor comprising contacting said cells with the OB derivative of claim 1.

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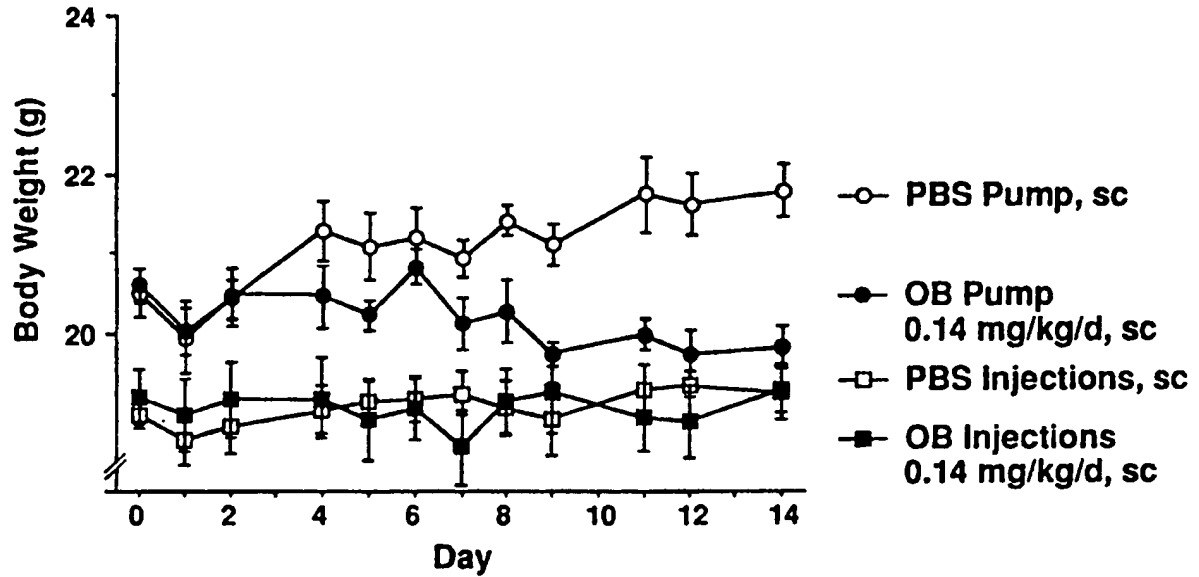


FIG. 1A

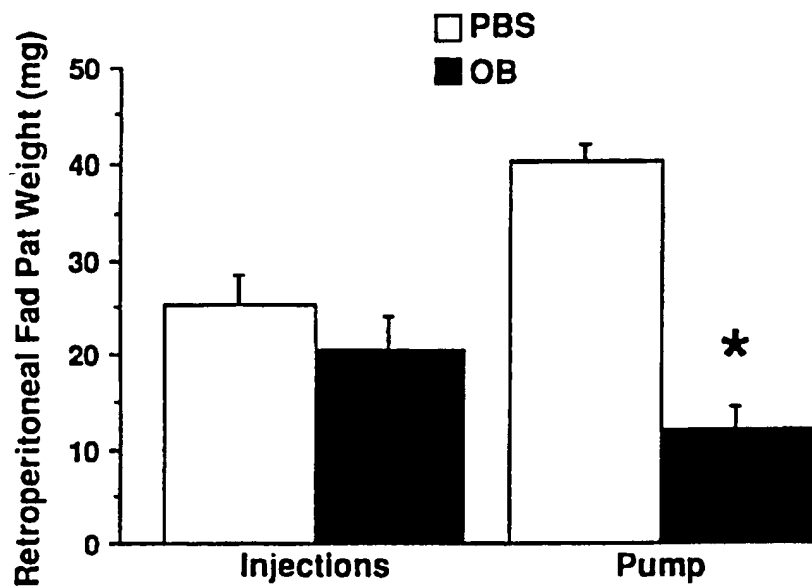


FIG. 1B

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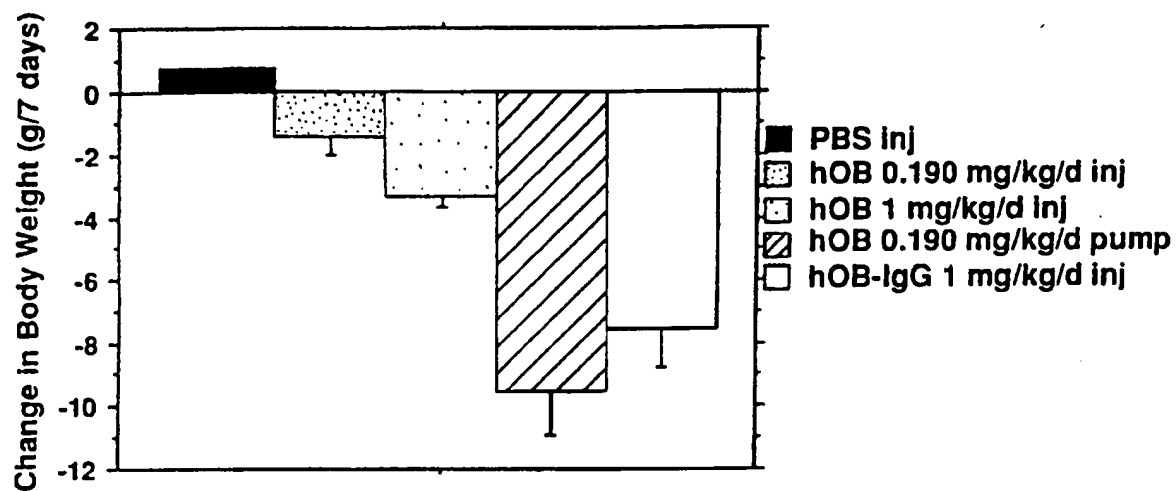


FIG. 2A

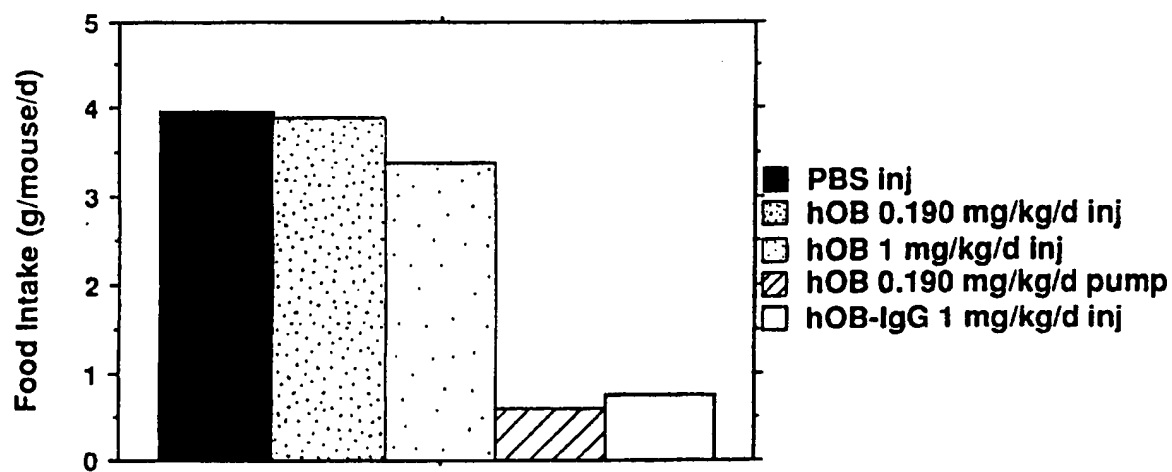


FIG. 2B

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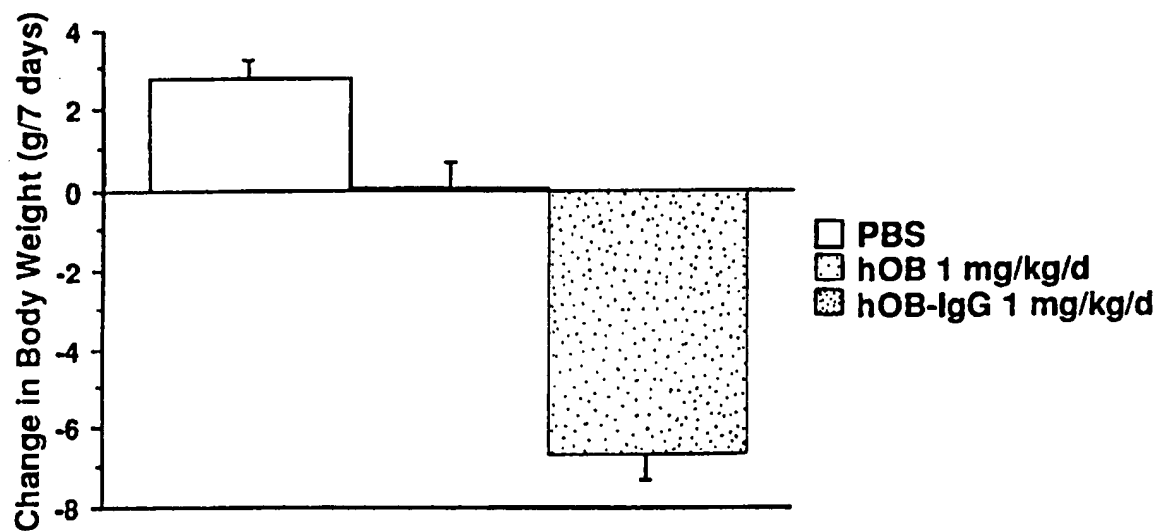


FIG. 3A

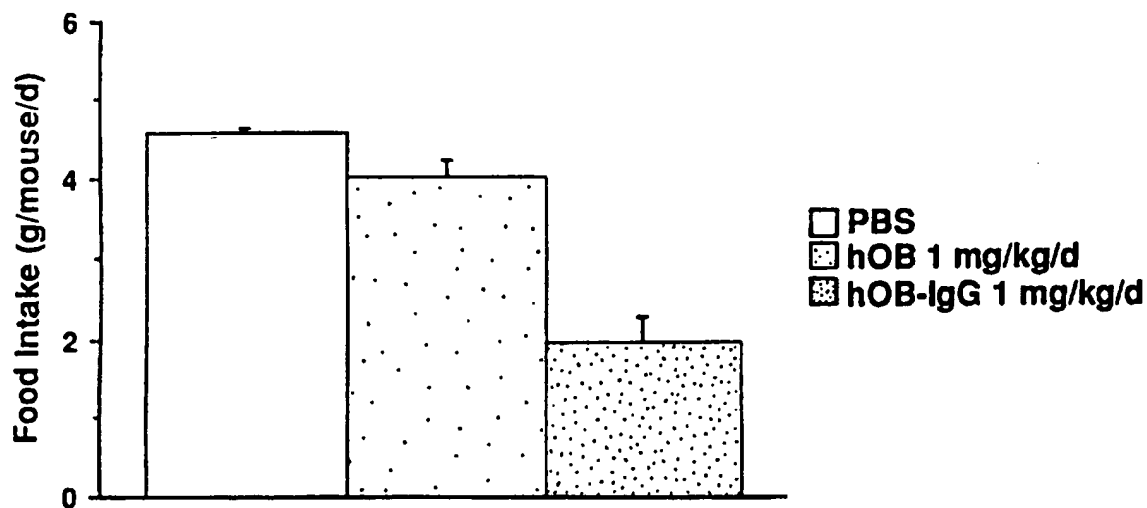


FIG. 3B

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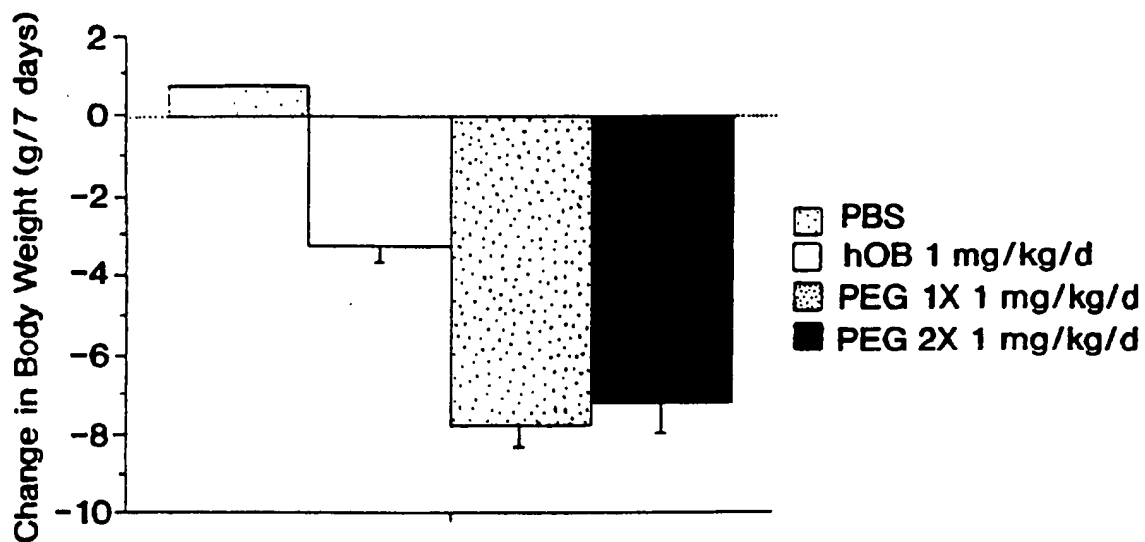


FIG. 4A

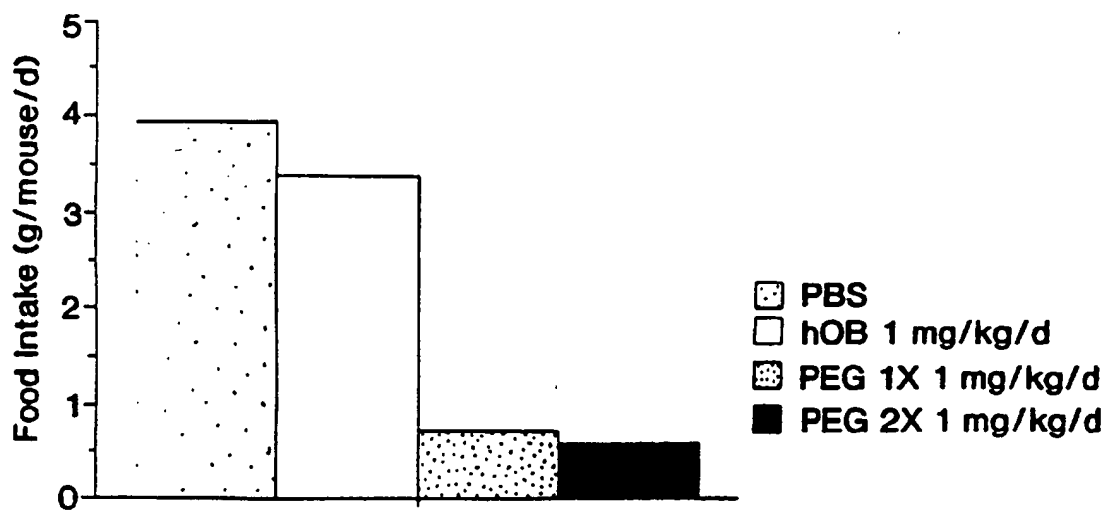


FIG. 4B

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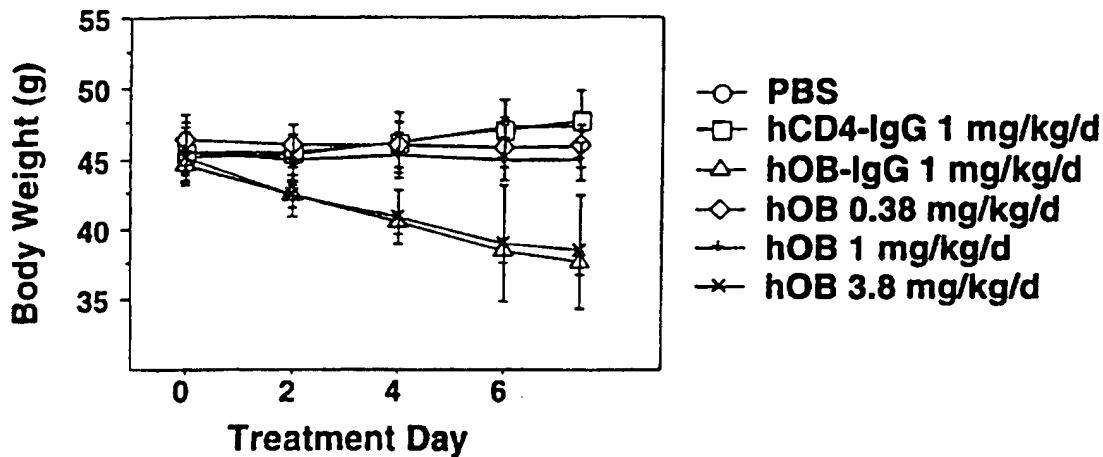


FIG. 5A

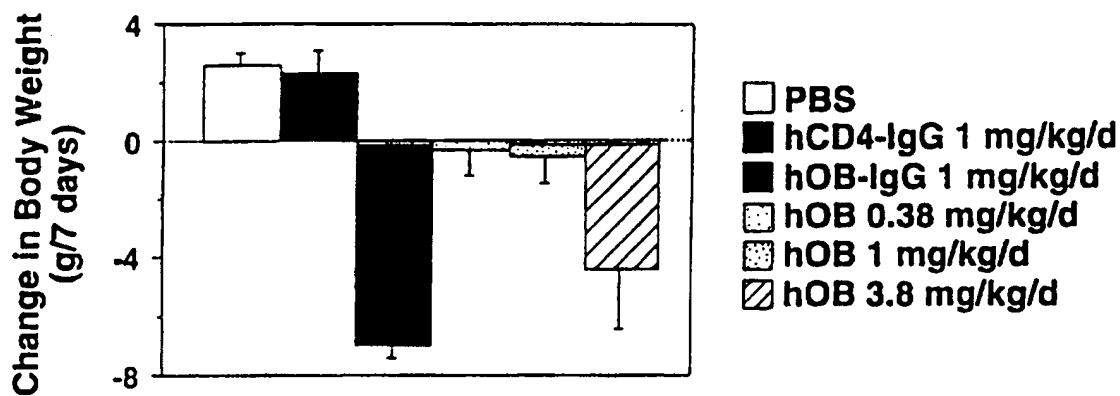


FIG. 5B

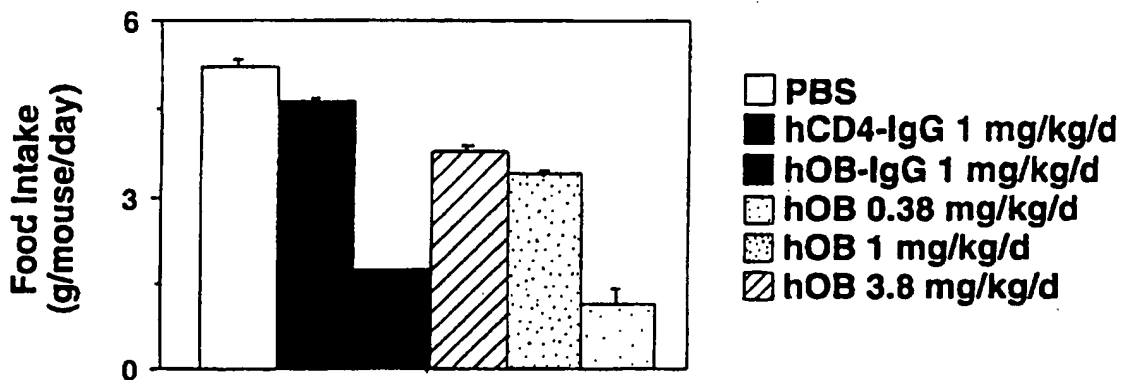


FIG. 5C

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```

> ss.pRK5tkneo.hOBlgC
> sites: std
> length: 7127 (circular)
> human OB Clat/BstEII cloning
> CHV enhancer/promoter

      aluI
      sstI
      sacI
      hgiI
      hgiAI/aspHI
      eciI36II
      bspl286
      bsiHKAI
      bmyI
      banII
      taqI
      rmaI      tru9I
      maeI      mseI
      speI      aseI/asnI/vspI
      1 TTGGAGCTCG CCGGACATTG ATTATTGACT AGTTATTAAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCCG GTTACATAAC
      AAGCTCGAGC GGGCTGTAACT TAATAACTCA TCAATAATTA TCATTAGTTA ATGCCCCAGT ATCAAGTAT CCGGTATATA CCTCAAGCGG CAATGTATTG
      thaI
      fnuDII/mvnI
      bstUI
      bsh1236I
      acII maeIII
      bslI
      101 TTACGGTAA TGGCGCGCT GGTGACCGC CCACGACCC CCGCCCATTC ACCTCAATAA TGACGTATGT TCCCATAGTA AGGCCAATAG GGACITTCOA
      AATGCCATTT ACCGGGGGA CCGACTGGCG GGTTCGTGGG GCGCGGTAAC TGCAGTTATT ACTGCATACA AGGTATCAT TCGGTTATC CTGAAAGGT
      maeII
      hnlI/acyI
      ahaII/bsaHI
      aatII
      201 TTGACGTCAA TGGGTGGAGT ATTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGA TCATATGCA AGTACGCC CTTATGACGT CAATGACCGT
      AACTGCAATT ACCCACTCA TAATGCCAT TTGACGGGTG AACCTCATG TAGTTCAAT AGTATACGT TCATCGCGG GATACTGCA GTTACTGCCA
      maeII
      hnlI/acyI
      ahaII/bsaHI
      aatII
      rsaI
      csp6I
      ndeI
      rsaI
      csp6I
      bglI
      maeII
      hnlI/acyI
      ahaII/bsaHI
      aatII

```

FIG. 6A

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```

scrFI
mvaI
ecorII
    aciI
        bglI dsav
        sau96I bstNI
        haeIII/palI
        asuI apyI(dcm+)
301 AAATGCCCCG CCGGCATTA TCCCGCATTA TCCCGCATTA TCCCGCATTA TCCCGCATTA TCCCGCATTA TCCCGCATTA
TTTACCGCGC GGACCGTAAT ACGGTCATG TACTGGAATA CCTGAAAGG ATGAACCGTC ATGTAGATCC ATATCAGTA GGATATCG TACCACCTAGC

        rsaI
        csp6I
        bsrI nlaIII
        rsaI snaBI
        csp6I bsaAI
        maeII
        styI
        nlaIII
        ncoI
        dsal hphI aciI
        bsaJI sfaNI

401 CGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGCA TTTCCCACTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA
CCAAACCGT CATGTATGTA CCGGCACCTA TCCCAAACT GAGTCCCTT AAGGTTTCAAG AGGTGGGTA ACTCCAGTTA CCTCAACA AAACCGTGGT

        rsaI
        csp6I
        pleI
        hinfI
        acII nlaIII
        bsmAI
        maeII
        hinfI/acyI
        ahaII/bsaHI
        aatII
        nlaIV
        hgiCI
        banI

501 AAATCAACGG GACTTTCCAA ATGTGCTAA CMACTCCGCC CCATTGACGC AAATGGGCGG TAGCGGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTGGT
TTTAGTTGCC CTGAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG GTTACCGGCC TTTACCGGCC ATCCGCACAT GCCACCTCC AGATATATTG GTCTCCAGCA

        maeIII
        aciI
        hgaI
        rsaI
        csp6I
        mnlI
        bsaII
        aluI
        sstI
        sacI
        hgiJII
        hgiAI/aspHI
        ecli36II
        bsp1286
        bsiHKAII
        bmyI
        banII

```

FIG. 6B

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```

        haeIII/palI
mcrI
eagI/xmaIII/ecI XI
eaeI
cfrI
fnu4HI
aciI
    thai
        fnuDII/mvni
        sacII/sstII
        nspBII
        kspI scrFI
        dsal nciI
        bglI bslI mspI
        sau3AI mnlI bstUI
        mboI/ndeII[dam-] hpaII
        dpnI[dam+] bsaJI dsav
        dpnII[dam-] bsh1236I
        alvi[dam-] aciI cauII
601 TTAGTGAACC GTCAGATGCC CTGAGAGCGC CATCCACGCT GTTTGACCT CCATAGAAGA CACCGGACC GATCCAGCT CCGCGCCCG GAAAGGTGCA
    AATCACTTGG CAGTCTAGCG GACCTCTCG GTAGTGCGA CAAAACTGGA GGTATCTTCT GTGCGCCTCG CTAGTCCGA GCGCGCGGCC CTGCCCACGT
    ~Begin RNA

        esp3I
        scrFI
        mvaI bsaAI
        ecoRII
        dsav
        bstNI hinII/acyI
        apyI[dcm+]
        sau3AI gsuI/bpmI
        mboI/ndeII[dam-]
        dpnI[dam+] hgaI fokI
        dpnII[dam-] ahaII/bsaHI
        mnlI
601 TTAGTGAACC GTCAGATGCC CTGAGAGCGC CATCCACGCT GTTTGACCT CCATAGAAGA CACCGGACC GATCCAGCT CCGCGCCCG GAAAGGTGCA
    AATCACTTGG CAGTCTAGCG GACCTCTCG GTAGTGCGA CAAAACTGGA GGTATCTTCT GTGCGCCTCG CTAGTCCGA GCGCGCGGCC CTGCCCACGT
    ~sp6 promoter

        tfII
        aciI
        thaI hinfi
        fnuDII/mvni
        bstUI
        bsh1236I
        maeII rsaI
        maeII csp6I
        maeII csp6I
        pleI scfI haeIII/palI
        scfI hinfi
        scfI hinfi
        asuI bsaJI
        asuI
        bstXI
        sau96I
        styI
        fnu4HI
        aciI
        thai
        fnuDII/mvni tru9I
        bstUI
        bsh1236I
        aaeI/asnI/vspI
701 TTGGAACCGG GATTCGCCGT GCCAAGAGTG ACGTAAGTAC CGCCTATAGA GTCTATAGCG CCACCCCTT GCCTTCGTTA GAACCGCGCT ACAATTAATA
    AACCTTCCG CTAGGGCGA CGGTCTCAC TGCATTGATG CGCGATATCT CAGATATCCG GGTGGCGGAA CCGAAGCAAT CTTCGCCGA TGTAAATTAT

```

FIG. 6C

[illegible]

FIG. 6D

[illegible]

FIG. 6E

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```

scrFI      eam11051
mvaI       sau96I
ecorII
dsav
bstNI
bsaJI      hphI      maeIII
          ddeI apyI(dcm+) maeIII
          mnlI bsaJI aciI baeIII
          1401 GACCTCAGCC CTGGTGGG GGTCAACGAC AAACTCACA CATGCCACAC GTGCCACCA CCTGAACTCC TGGGGGACC GTCAGTCTTC CTCTTCCCCC
          CTGGAGTGG GACCAACGCC CCAGTGGCTG TTTTCACTGT GTACGGGTGG CACGGGTCTG GGACTTCAGG ACCCCCTGG CAGTCAGAAG GAGAAGGGGG
          162 AspLeuSerP roGlyCysG1 yValThrAsp LysThrHisT hrCysProAla ProGluLeuL euGlyGlyPr oSerValPhe LeuPhePr Pr
          ^insertion of a gly
          ^START OF HUMAN IgG1 CH2CH3

          sau96I
          nlaIV
          mspI
          hpall
          scrFI
          nciI
          dsav
          sauJAI avall
          mboI/ndeII(dam-) nlaIII
          nlaIII caulI mnlI nspl
          rcaI dpaI(dam+) ddeI nsphI
          bspHI(dam-) asuI eco8II maeIII
          mnlI dpaII(dam-) bsu36I/mstII/sauI maeII
          styI      1501 CAAACCCAA GCACACCTC ATGATCTCC GCACCCCTGA GGTACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCCT GAGGTCAAGT TCAACTGCTA
          bsaJI      GTTTTGGTT CTGTGGGAG TACTAGAGG CCTGGGACT CCAGTGTACG CACCACCACC TGCACCTCGT GCTTCTGGGA CTCACGTTCA AGTTGAGCCAT
          196 LysProLy sAspThrLeu MetIleSera rgThrProG1 uValThrCys ValValVala spValSerHI sGluAspPro GluValLysP heAsnTrpTyr

```

FIG. 6F

[illegible]

FIG. 6G

FIG. 6H

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```

sau3AI
mboI/ndelI[dam-]
dpsI[dam+]
dpsII[dam-]
pvuI/bspCI
acrI
    taqI[dam-] tru9I
    clai/bsp106[dam-]
sau3AI mseI
mboI/ndelI[dam-]
dpsI[dam+] xmnI
dpsII[dam-] asel/asnI/vsPI bsaJI
    alaIII alvi[dam-] asp700 hhal/cfoI nlaIII mnlI
2301 CTTATCATGT CTGCATCGAT CGGGAATTAA TTCCGCCGAC CACCATGGCC TGAATAACCC TCTGAAGAG GAACTTGGTT AGGTACCTTC TGAGCGGGA
    GAATAGTACA GACCTAGCTA GCCCTTAATT AAGCCCGCTC GTGGTACCGG ACTTTATTGG AGACTTTCTC CTTGAACCAA TCCATGCAAG ACTCGGCTT
    ~sv40 origin

    rsaI
    csp6I
    nlaIV
    kpnI
    hgiCI
    banI
    asp718 mnlI
    acc65I ddeI acII
2401 AGAACCAAGCT GTGCATCTG TGTCACTTAG GGTGTGGAAA GTCCCCAGGC TCCCAGCAGG GCAGAGTAT GCAAGCATG CATCTCAATT AGTCAGCAAC
    TCTTGTTGCA CACCTACAC ACAGTCATC CCACAGCTTT CAGGGTCCG AGGGTCTGC CGTCTTCATA CGTTCTGATC GTAGATTAA TCACTGCTTG
    aluI
    pvuII
    nsp8II
    nlaIV
    scrFI
    mvaI
    ecorII
    dsav
    bstNI
    apyI[dcM+]
    bsaJI
    sfaNI
    ppulOI
    nsiI/avaIII
    nlaIII
    sphi
    nspI
    nspHI
    scrFI
    mvaI
    ecorII
    dsav
    bstNI
    apyI[dcM+]
    sexAI
2501 CAGGTGTGGA AGTCCCCAG GCTCCCCAGC AGGCAGAGT ATGCAAGCA TGCATCTCAA TTAGTCAGCA ACCATAGTCC CCCCCCTAAC TCGGCCATC
    GTCCACACCT TTCAGGGGTC CGAGGGGTGC TCGTCTTCA TACCTTCTGT ACGTAGATT ATCAGTCTGT TCGTATCAGG GCGGGGATTC AGCGCGTAG
    nlaIV
    scrFI
    mvaI
    ecorII
    dsav
    bstNI
    apyI[dcM+]
    bsaJI
    nlaIV
    scrFI
    ppulOI
    nsiI/avaIII
    nlaIII
    sphi
    nspI
    nspHI
    sfaNI
    acII
    foki
    acII

```

FIG. 6I


```

fnu4HI
bglI
sfII
haeIII/palI
mnlI mnlI ddeI
haeIII/palI bsaJI mnlI aluI
mnlI bsaJI acII haeIII/palI
ATTATCGCAG AGGCCGAGGC CGCTCGGCC TCTGACCTAT
TCCGCTCCG GCGGACCCG AGACTCGATA
2601
nlaIII
styI
ncol
bslI dsal
acII bsaJI
bsaI acII acII
CTCGGCCAG TTCCGCCAT TCTCGCCCC ATGGTCACT AATTTTTT
ATTCGACTG TTAATAAAA TAAATACCTC TCCGCTCCG
GCGGACCCG AGACTCGATA
2701
styI
bsaJI
blnI
haeIII/palI
stul rmaI
hael mael
mnlI mnlI avrII
TTTTTGGAG CCTAGGCTT TTGCAAAAAG CTGTTAATC
GAACACGCAG ATGCACTCGG GCGGCGCGG TCCACGTCG
AGGCTTCTAT CACTCTCCG AAAAACCCTC CGATCCGAA
AACGTTTTTC GACAATTAG CTGTGCGTC TACGTACGCC
CGCGCGCGC AGGCTCCAGC
~start pUC118
~TK promoter
sauJAI
mboI/ndeII(dam-)
dpmI(dam+)
sauJAI
mboI/ndeII(dam-)
dpmI(dam+)
bstYI/xhoII
bglII dpmII(dam-)
bglII hincII/hindII acII dpmII(dam-) bsaJI
acII msel hgaI fnu4HI bclII(dam-)
TCACACCGT TCACACGATC TGATCAGAG
CGGCTGCGC GAATGTGCG AGTTGCGCA CGGCTGCTAG
ACTAGTCTC
tms neomycin phosphotransferase gene.

```

FIG. 6J

FIG. 6K

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```

scrPI      sau3AI      fnu4HI      sau3AI
ncII       mboI/ndelII(dam-)      mboI/ndelII(dam-)
mspI       dpnI(dam+)      dpnI(dam+)
hpaII      dpnII(dam-)      dpnII(dam-)
dsav       bstXI/xhoII      alvi(dam-)
cauII      alvi(dam-)      hphI
bsaJI      hphI
3201 TTGGGGCAAG TGCGGGGCA GATCTCTG TCATCTCACC TTGCTCTCC CGAGAAAGTA TCATCATGG CTGATGCAT GCGGGGCTG CATACGCTTG
AACCGGCTT CAGCGGCGT CTTAGAGGAC AGTAGAGTGG AACGAGGAGG GCTCTTTCAT AGGTAGTACC GACTAGCTTA CCGCGCGGAC GTATGCCAAC

          nlaIII sfaNI
          acII bbvI
          fnu4HI
          fnu4HI
          fnu4HI
          mboI/ndelII(dam-)
          dpnI(dam+)
          dpnII(dam-)
          earI/ksp632I
          foki
          sau3AI dpnI(dam+)
          mboI/ndelII(dam-)
          dpnI(dam+)
          dpnII(dam-)
          taqI(dam-)
          dpnII(dam-)
          foki
          cfr10I
          taqI(dam-)
          dpnII(dam-)
          GATCGGAGC
          GCGTCTTGTG
          GATCAGGATG
          ATCTGGACCA
          TAGCGGATG
          GACGGGTAG
          CTGCTGCTTC
          GCTTTGTAGC
          GTAGCTGCT
          CTGCTATCAG
          CCTACTTCC
          GCCAGAACAG
          CTAGTCTTAC
          TAGACCTGCT

          rsaI
          csp6I
          bsaAI
          hgiAI/asphI
          bsp1286
          taqI bsiHKAII
          sfaNI
          bmyI maeII
          foki
          GATCGGAGC
          GCGTCTTGTG
          GATCAGGATG
          ATCTGGACCA
          TAGCGGATG
          GACGGGTAG
          CTGCTGCTTC
          GCTTTGTAGC
          GTAGCTGCT
          CTGCTATCAG
          CCTACTTCC
          GCCAGAACAG
          CTAGTCTTAC
          TAGACCTGCT

          sphI
          nspI
          nspHI
          hinPI
          hhaI/cfoI
          hlnPI
          thal
          fnuDII/mvni
          bstUI
          hgiJII
          bsp1286
          bmyI bsh1236I
          banII hhaI/cfoI
          sfaNI
          GATCGGATCAG
          GCGTCTGCGC
          CAGCGGAAT
          GTTGGCCAG
          CTCAGGCGC
          GCATGCCGA
          CCGCGGAGAT
          CTGCTGTGCA
          CCGATGCCGA
          TGCGTGTGTTG
          TCTGTAGTC
          CCGAGCGCG
          GTGGCTTGA
          CAAGCGTCC
          GAGTTCCCG
          CTTACGGCT
          GCGCTCTTA
          GACGAGCACT
          GGGTACCGCT
          ACCGAGCAAC

          sau3AI
          mboI/ndelII(dam-)
          dpnI(dam+)
          dpnII(dam-)
          alvi(dam-)
          foki
          sau3AI dpnI(dam+)
          mboI/ndelII(dam-)
          dpnI(dam+)
          dpnII(dam-)
          earI/ksp632I
          foki
          sau3AI dpnI(dam+)
          mboI/ndelII(dam-)
          dpnI(dam+)
          dpnII(dam-)
          taqI(dam-)
          dpnII(dam-)
          foki
          cfr10I
          taqI(dam-)
          dpnII(dam-)
          GATCGGAGC
          GCGTCTTGTG
          GATCAGGATG
          ATCTGGACCA
          TAGCGGATG
          GACGGGTAG
          CTGCTGCTTC
          GCTTTGTAGC
          GTAGCTGCT
          CTGCTATCAG
          CCTACTTCC
          GCCAGAACAG
          CTAGTCTTAC
          TAGACCTGCT

          sphI
          nspI
          nspHI
          hinPI
          hhaI/cfoI
          hlnPI
          thal
          fnuDII/mvni
          bstUI
          hgiJII
          bsp1286
          bmyI bsh1236I
          banII hhaI/cfoI
          sfaNI
          GATCGGATCAG
          GCGTCTGCGC
          CAGCGGAAT
          GTTGGCCAG
          CTCAGGCGC
          GCATGCCGA
          CCGCGGAGAT
          CTGCTGTGCA
          CCGATGCCGA
          TGCGTGTGTTG
          TCTGTAGTC
          CCGAGCGCG
          GTGGCTTGA
          CAAGCGTCC
          GAGTTCCCG
          CTTACGGCT
          GCGCTCTTA
          GACGAGCACT
          GGGTACCGCT
          ACCGAGCAAC

```

FIG. 6L

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```

          mspI      bslI
          hpall     sau96I
          nael      avall
          cfrI0I    asul
          haeIII/palI  rsrII/cspI
          eaeI      cpol
          tflI      acII acII
          hinfI     cfrI
          taqI      cfrI
          nlaIII
3501 CCGAATATCA TGGTGGAAA TGGCGCTTT TCTGGATTCA TCGACTGTGG CCGGCTGGGT GTGGCGGACC GGTATCAGGA CATAGCGTTG GCTACCCGTG
    GGCTTATAGT ACCACCTTTT ACGCGGAAA AGACCTAAGT AGCTGACACC GCGGACCCA CACCGCTGG CGATAGTCTT GTATCGCAAC CGATGGGCAC

          sapi      hinfI
          mboII     fnu4HI
          earI/kpf32I
          eco57I aluI acII
3601 ATATTGCTGA AGAGCTTGGC GCGGAATGGG CTGACCGCTT CTCTGTGCTT TAGGTTATCG CCGCTCCCA TTGCGAGCGC ATGCGCTTCT ATGCGCTTCT
    TATACGACT TCTCGAACC CCGCTTACC GACTGGCGA GAGTGGCGA GGAGCAGCAA ATGCCATAGC GCGAGGCT AGCGTGGC TAGCGGAAGA TAGCGGAAGA

          taqI
          sfuI
          bstBI
          bsiCI
          asuII
          acII      pleI
          ddel      bsrBI hinfI
          mboII     bsrBI hinfI
3701 TGACGAGTTC TTCTGAGCGG GACTCTGGG TTGGAATGA CCGACCAAGC GAGCCCAAC CTGCCATCAC GAGATTGCA TTCCACGCC GCGTCTTATG
    ACTGCTCAG AGACTGGC CTGAGACCC AGCTTTACT GGTGGTTG GCGGTAGT GCGGTAGT CTCTAAGT AGGTGGCG CGGAGATAC

```

FIG. 6M

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acII
 thal
 fnuDII/mvni
 bstUI
 sacII/sstII
 haeIII/palI bsh1236I
 mcrI nsp8II
 dsal kspI
 bsajI dsal
 hphI eagI/xmaIII/ecI XI
 maeIII eaeI bsajI
 bsteII cfrI acII
 4401 CGCGCCGGAC GAACATAACC TGACTAGCGC ATCTCTGCC CTCTTCCT GGTACGAGGA CGCTTTTGT TTTGTATTGG TCACGACGGC CGAGTTTCCG
 CGCGCCGCTG CTGATTGG ACTGATGCGG TAGACAGCGG GAAGAAGCGA CCATGCTCT CT CGCAAAACA AACATAACC AGTGTGCGG GCTCAAGGC
 mspI
 hpall
 acII
 fnu4HI
 bsII sfaNI
 mboII
 rsaI haeII
 mnlI hhaI/cfoI
 hlnPI
 hhaI/cfoI
 csp6I eco47III
 4501 CGCGACCCCG GCGAGGCGAC CTGTCTTAGC AGTTGCATGA TAAAGAAGAC AGTCATAAGT GCGCGACGA TAGTCATGCC CCGCGCCAC CGGAAGGAGC
 CGCTTGGGC CGTCCCGT GACAGGATGC TCAAGCTACT ATTTCTTCTG TCAGTATTC ACGCGCTGCT ATCAGTACGG GCGCGGGTG GCTTCTCTG
 *pBR322 sequence
 scrFI nlaIV
 nciI hgiCI
 dsav scrFI
 caulI mvaI
 bslI ecoRII
 bslI dsav
 bsajI bstNI
 sau96I bsajI
 nlaIV haeIII/palI
 avall eaeI
 asul cfrI bsp1286
 ppuHI mspI apyI(dcm+)
 nlaIV hpall bayI
 eco0109I/draII bnl
 4501 CGCGACCCCG GCGAGGCGAC CTGTCTTAGC AGTTGCATGA TAAAGAAGAC AGTCATAAGT GCGCGACGA TAGTCATGCC CCGCGCCAC CGGAAGGAGC
 CGCTTGGGC CGTCCCGT GACAGGATGC TCAAGCTACT ATTTCTTCTG TCAGTATTC ACGCGCTGCT ATCAGTACGG GCGCGGGTG GCTTCTCTG
 hlnPI mspI
 hhaI/cfoI
 hpall
 fnuDII/mvni
 bstUI bsawI
 bsh1236I
 thal
 nlaIII acII bslI
 aluI
 fnu4HI
 acII bcgI
 nlaIII
 mboII
 bpuAI
 bbsI
 nlaIII
 4501 CGCGACCCCG GCGAGGCGAC CTGTCTTAGC AGTTGCATGA TAAAGAAGAC AGTCATAAGT GCGCGACGA TAGTCATGCC CCGCGCCAC CGGAAGGAGC
 CGCTTGGGC CGTCCCGT GACAGGATGC TCAAGCTACT ATTTCTTCTG TCAGTATTC ACGCGCTGCT ATCAGTACGG GCGCGGGTG GCTTCTCTG
 *pBR322 sequence

FIG. 6P

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```

fnu4HI          acII
haeIII/palI    fnu4HI
mcrI            thal
eagI/xmaIII/ecI XI  fnuDII/mvni
eseI            bstUI
notI            hinPI
fnu4HI          fnuDII/mvni
aciI            bstUI
mcrI bsrBI aciI  hinPI
sfanI taqI cfrI sfaNI  hhaI/cfoI hhaI/cfoI
GTCGAGCGGC CGCATCAAG CAACCATAGT ACGCCCTCTG TAGCGGGCGA TTAGCGCGG CGGGTGTGGT
ACTGACCCAA CTTCGAGAG TTCCGTAGC CAGCTGCGC GCGTAGTTTC GTTGGTATCA TCGCGGGGAC ATCGCGCGCT AATTCGCGCC GCCACACCA
~delta 3
^M13 ori

fnu4HI          mspI
hinPI           hpaII
hhaI/cfoI       nseI
thal            maeII cfrI01
fnuDII/mvni     bsh1236I
bstUI           bsh1236I
bsh1236I        maeII
maeIII bbvI maeII  GGTACGCGC AGCGTGACCG CTACACTTGC CAGCGCCCTA GCGCCGCTC CTTTGGCTT CTCCCTTCC TTCTCGCCA GGTTCGCGC CTTTCCCGT
CCAAATGCGC TCGCACTGCC GATGTGACG GATCGGGCAT GCGGGCGAG GAAGCGAA GAAGCGAGC AAGAGCGCT GCAAGCGCC GAAAGGGGCA

nlaIV           maeII haeIII/palI
hg1JII          draIII sau96I
bap1286         bsaAI asuI
bmyI            hphI
banII           hphI
aluI            hphI
4801 CAAGCTCTAA ATCGGGGCGT CCCTTTAGG TTCCGATTTA GTGCTTTAGG GCACCTGCAC CCCAAAAC TTGATTTGG TGATGTTCA CGTAGTGGC
GTTGAGATT TAGCCCCCA GGGAAATCC AGGCTAAT CAGGAATGC CGTGGAGCTG GGGTTTTTG AACTAAACC ACTACCAAGT GCATCACTCG

maeII pleI      bslI
drdI hinfi maeII bsrI
4901 CATGCCCTG ATGACGGTT TTGCGCTT TGACGTGCA GTCCAGCTTC TTTAATAGT GACTTTGTT CCMACTGGA ACMACTCA ACCCTATCTC
GTAGCGGCAC TATCTGCCA AAGCGGGA ACTGMACT CAGGTGCAAG AATTATCAC CTGAGAACAA GGTTCACCT TGTGTGAGT TGGATAGAG

```

FIG. 6Q

5001 GGGCTATTCT TTGATTTAT AAGGATTTT GCGATTTTG CCTATTGCT TAAAAATGA GCTGATTAA CAAAAATTA ACGCAATTT TAACAAATA
 CCGGATAAGA AACTAATA TTCCCTAAA CCGCTAAGC CGGATAACCA ATTTTACT CGACTAAAT GTTTTAAAT TGGCTTAAA ATTGTTTAT
 maeli mni haeli/pali tru9I msel
 psp14061 haeli/pali tru9I msel
 tru9I stuI haeli
 msel haeli
 5101 TTAACGTTA CAATTTATG GTGAGCGCT CGTGATCGC CTATTTTAT AGTTAATGT CATGATAATA ATGGTTTCT ACAGCTCAGC TGGCACTTTT
 AATTGCAAT GTTAAATAC CACGTCGGA GCACTATGC GATAAATA TCCATTTACA GTACTATTAT TACCAAGAA TCTGCAGTCC ACCGTGAAA
 maeli nlaII nlaII rcal msel bspHI ddel aatII
 hiniI/acyI
 ahalI/bsaHI
 5201 CGGGGAATG TCGCGGAAC CCTATTGT TATTTTCT AATACATC AATATGTAT CCGCTCATGA GACAATAAC CTGATTAATG CTTCNAATAT
 GCCCCTTAC ACCGCTTG GGGATAACA AATAAAGA TTTATGTAG TTTATACATA GCGAGTACT CTGTATTG GACTATTAC GAAGTTATA
 rcal bspHI bsrBI bsmAI acII nlaIII
 5301 ATTGAAAAG GAAGATATG AGTATTCAC ATTCCGTG TCCCTTAT CCGCTTTTG CGGCATTTG CCTTCTGTT TTGCTCACC CAGNAACGCT
 TAACTTTTC CTTCATAC TCATAGTTG TAAGGCACA CCGGAATAA CCGGAANAAC GCGTAANAAC GGAAGGACAA AAGGAGTGG GTCTTTGGA
 mboII fnu4HI acII hphI
 earI/asp632I
 5401 GGTGAAAGTA AAGATGCTG AAGATCAGTT GGTGTCACGA GTGGGTTACA TCGAAGTGA TCTCAACAGC GGTAAATCC TTGAGAGTTT TCGCCCCGAA
 CCACTTTTAT TTCTACGAC TTCTAGTCAA CCCACGTGCT CACCAATGT ACCTTGACT ACAGTTGTCG CCATTCTAGG AACTCTCAA ACGGGGCTT
 hphI eco57I apaLI/snoI bsrI nsp8II alviI/dam-] bstyI/xhoII
 sfaII mboII[dam-] alw4I/snoI maeliI taqI alviI[dam-] acII bstyI/xhoII
 sau3AI mboI/ndelI[dam-] dpnI[dam+] dpnII[dam-] bstyI/xhoII
 sau3AI mboI/ndelI[dam-] dpnI[dam+] dpnII[dam-] bstyI/xhoII
 hgiAI/aspHI bsp1286 bsiHKAI
 sau3AI mboI/ndelI[dam-] dpnI[dam+] bmyI
 dpnII[dam-]

FIG. 6R

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scrFI
 nciI
 mspI
 hpaII
 dsav
 caulI
 hinII/acyI
 hgaI
 acII
 mcrI fnu4HI
 bcoGI
 ahaII/bsaHI
 gntACGCCG GCGAAGACCA ACTCGGTGGC CGCATACACT
 5501 GAACGTTTTT CAATGATCAG CACTTTTAA GTTCTGCTAT GTGGCGCGT ATTATCCCGT CATGACGCCG GCGAAGACCA ACTCGGTGGC CGCATACACT
 CTTGCAAAAG GTTACTACTC GTGAAATTT CAAGACGATA CACCGCGCA TAATAGGCA CTACTGCGC CGTTCTCTT TGAGCCAGCG CGGTATGTGA

 rsaI
 csp6I bsrI
 scaI hphI maeIII sfaNI foki nlaIII
 ddeI
 5601 ATTCTCAGAA TGACTTGTT GAGTACTCAC CAGTCACAGA AAGCATCTT ACGGATGCCA TGACAGTACG AGAATTATCC AGTCTGCGCA TAACCATGAG
 TAAAGTCTT ACTGAACCAA CTCATGAGTG GTCATGTCT TTTCTAGAA TGCCTACCGT ACTGTCATTC TCTTAATACG TCACGACCGT ATTGCTACTC

 sau96I
 avaiI
 sau3AI asuI
 mboI/ndeII[dam-]
 dpnI[dam+]
 dpnII[dam-]
 pvuI/bspCI
 mcrI mniI
 aluI acII
 5701 TGATAACACT GCGGCCAAT TACTTCTGAC AACGATCGA GGACCGAGG AGCTAACCGC TTTTTCAC AACATGGGG ATCATGTAC TCGCCCTGAT
 ACTATTGTGA GCGCGGTGA ATGAGACTG TTGCTAGCCT CTGCTTCC TCGATTGCGG AAAAAAGTG TTGTACCCC TAGTACATG AGCGAACA

 mspI
 hpaII
 bsaHI
 nlaIV aluI
 maeIII sfaNI
 fnu4HI bsvI
 avIII/fspI
 maeII hhaI/cfoI
 pspl406I
 mcrI
 5801 CGTTGGGAC CGGAGCTGA TGAGCCATA CCAAGCAGC AGCTGACAC CAGGATGCCA GCAGCATGG CACACAGCTT GCGCAACTA TTAACGGCG
 GCAACCCCTG GCGTGCATCT ACTTCGGTAT GGTTCGCTG TCGCACTGTG GTGCTACGCT CGTCTTACC GTTCTGCA CGGCTTGT ATTGACCGC

FIG. 6S

FIG. 6T

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```

sau3AI
mbol/ndelII[dam-]
dpnI[dam+] sau3AI          thaI
dpnII[dam-] mbol/ndelII[dam-]
bstYI/xhoII dpnI[dam+] fnuDII/mvnI
sau3AI alwI[dam-] dpnII[dam-] bstUI
mbol/ndelII[dam-] alwI[dam-] bsh1236I
dpnI[dam+] mboII[dam-] hinPI fnu4HI
dpnII[dam-] bstYI/xhoII hhaI/cfoI bbvI
ddel hgaI
6301 TTGGTTCCAC TGAGCGTCAG ACCCGTAGA AAGATCAAA GGATCTTCTT TTTTCTGCGC GTATCTGCT GCTTGCAAC AAAAAACCA
AAGCAAGGTG ACTCCAGTC TGGGCACTT TTTCTAGTTT CCTAGAAGAA CTCTAGCAA AAAGACGCG CATTAGCGA CGACGTTTG TTTTTTGGT

sau3AI
mbol/ndelII[dam-]
dpnI[dam+]
dpnII[dam-]
alwI[dam-]
mspI
hpaII
alul
6401 CCGTACCG CCGTGGTTG TTTCGGCAT CACAGCTAC CAACCTTTT TCCGAGGTA ACTGCTTCA GCAGAGCGCA GATACCAAT ACTGCTCTTC
CGCATGGTC GCGACCAAG CACCGGCTA GTTCTCGATG GTTGAGAAA AGCTTCCAT TGACCGAAGT COTCTCGCT CTATGGTTA TGACAGGAAG

haeIII/palI
baII haeI
6501 TAGTGTAGCC GTAGTAGGC CACCACTTCA AGAATCTGT AGCACCGCT ACATACCTCG CTCTGCTAAT CCGTTTACCA GTGGCTGCTG CCAGTGGCGA
ATCACATCG CATCATCCG GTGGCAAGT TCTTGAGACA TCGTGGCGCA TGTATGAGC GAGAGCATTA GGACAAATGT CACCGACGAC GGTCAACGGT

scrFI
ncII
mspI
hpaII
dsav
cauII
pleI
hinfi
6601 TAAGTGGTGT GTTACCGGT TCGACTCAG ACCATAGTTA CCGGATAAGG CCGACCGCTC GGCTGAACG GGGGTTGCT GCACAGCC CAGCTTGGAG
ATTGAGCACA GAATGGCCA ACCTGAGTTC TGTATCAAT GCGCTATCC GCGTGGCAG CCGACTTGC CCCCCACCA CGTGTGCTGG GTCCAACTTC

hgIAI/aspHI
bsp1286
bsiHKAII
bmyI
apaLI/enol
alv44I/enol
alul

```

FIG. 6U

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/20718

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/16 C07K14/575 A61K38/22 C12N15/70 C12N1/21 //(C12N1/21,C12R1:19)		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K C12N A61K		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 97 00319 A (SMITHKLINE BEECHAM PLC ;BROWNE MICHAEL JOSEPH (GB); CHAPMAN CONRAD) 3 January 1997 see page 1, line 31 - line 33; claims; examples	1-4,7-26
P,X	--- EP 0 741 187 A (HOFFMANN LA ROCHE) 6 November 1996 see page 9, line 19 - page 11, line 46; claims; examples 19,20	1-3, 6-12,26
P,X	--- WO 96 05309 A (UNIV ROCKEFELLER ;FRIEDMAN JEFFREY M (US); ZHANG YIYING (US); PROE) 22 February 1996 see page 43, line 3 - page 46, line 14; claims	1-3, 6-12,26
--- -/--		
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 17 April 1997		Date of mailing of the international search report 14. 05. 97
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016		Authorized officer Fuhr, C

INTERNATIONAL SEARCH REPORT

Inter-
national Application No
PCT/US 96/20718

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>NATURE, vol. 372, no. 6505, 1 December 1994, pages 425-432, XP000602062 YIYING ZHANG ET AL: "POSITIONAL CLONING OF THE MOUSE OBESE GENE AND ITS HUMAN HOMOLOGUE" see the whole document -----</p>	<p>1,10-12, 26</p>

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/ 20718

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 7-10, 24-25
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 7-10, and 24-25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Inter. Application No

PCT/US 96/20718

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9700319 A	03-01-97	AU 6011096 A	15-01-97
EP 0741187 A	06-11-96	AU 5197896 A	14-11-96
		CA 2175298 A	06-11-96
		ES 2093593 T	01-01-97
		JP 9003098 A	07-01-97
		NO 961796 A	06-11-96
		PL 314051 A	12-11-96
WO 9605309 A	22-02-96	AU 3329895 A	07-03-96
		CA 2195955 A	22-02-96
		DE 19531931 A	07-03-96
		FI 970656 A	17-02-97
		GB 2292382 A	21-02-96
		JP 9502729 T	18-03-97
		ZA 9506868 A	09-04-96